

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:51:54 ; Search time 21 Seconds
(Without alignments)
1716.686 Million cell updates/sec

Title: US-09-839-185-2

Perfect score: 2040
Sequence: 1 MEMGNSGPGHGPQAGSGG.....MEDENTRAYDSSSHHTNWSL 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2033	99.7	375	2	T00929
2	1956	95.9	373	2	T52553
3	863.5	42.3	354	2	T46014
4	615	30.1	323	2	T52297
5	556	27.3	257	2	T52298
6	400	19.6	425	2	T52604
7	392	19.2	419	2	T52603
8	374.5	18.4	405	2	T52552
9	356	17.5	396	2	T52556
10	354.5	17.4	389	2	B86359
11	354.5	17.4	393	2	T52558
12	333	16.3	333	2	T52594
13	330	16.2	171	2	T52607
14	330	16.2	181	2	T52607
15	328.5	16.1	1020	2	H96793
16	321.5	15.8	138	2	T52567
17	321	15.7	927	2	T47827
18	318.5	15.6	1035	2	G86342
19	313	15.3	305	2	T52299
20	310	15.2	881	2	T52601
21	309	15.1	881	2	T52602
22	308.5	15.1	131	2	T04328
23	305	14.9	167	2	T52599
24	303.5	14.9	167	2	T52599
25	303.5	14.9	174	2	T02160
26	297	14.6	240	2	T02160
27	292.5	14.3	129	2	H84749
28	292.5	14.3	131	2	T52597
29	255.5	12.5	377	2	T52606

30	254.5	12.5	801	2	T52605	squamosa promoter
31	160.5	7.9	1043	2	T13733	FT2-F1 protein - F
32	157.5	7.7	331	2	G96785	protein-tyrosine k
33	152	7.5	1584	2	T18276	1-phosphatidylinos
34	146	7.2	1858	2	T18273	BRCore-NS-23 prote
35	145	7.1	704	2	S21911	hypothetical prote
36	140	6.9	695	2	T21950	gene mastermind pr
37	129	6.3	1555	2	T13998	trifa protein - sil
38	127	6.2	602	2	F84432	steroid hormone re
39	126	6.2	1390	2	T14004	ecdysose-inducible
40	126	6.2	1748	2	S42136	probable Gr-like t
41	125	6.1	647	2	S05450	serine/threonine p
42	125	6.1	864	2	A49070	cell division cont
43	124.5	6.1	603	2	F96797	
44	124	6.1	1230	2	T18259	
45	123.5	6.1	758	2	S45825	

ALIGNMENTS

RESULT 1

T00929
squamosa-promoter binding protein 9 [imported] - Arabidopsis thaliana

N/Alternate names: transcription factor sp19

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 23-Mar-2001

C/Accession: T00929; T52595; A84851

R/Rounley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, December 1997

A/Description: Arabidopsis thaliana chromosome II BAC T4P15 genomic sequence.

A/Reference number: Z14212

A/Accession: T00929

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-375 <ROU>

A/Cross-references: EMBL:AC002561; NID:g2673901; PID:g2673911

A/Experimental source: cultivar Columbia

R/Caron, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.

Gene 237, 91-104, 1999

A/Title: Molecular characterisation of the Arabidopsis SBP-box genes.

A/Reference number: Z25236; WUID:99453765; PMID:10524240

A/Accession: T52595

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-375 <CAR>

A/Cross-references: EMBL:AD011638; PIDN:CAB56590.1

A/Experimental source: cultivar Columbia; tissue type inflorescence

R/Lin, X.; Kaul, S.; Rounley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; WUID:20083487; PMID:10617197

A/Accession: A84851

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: GB:AE002093; NID:g2673911; PIDN:AAB8645.1; GSPDB:GN00139

C/Genetics:

A/Gene: sp19; T24P15.11; AC2942200

A/Map position: 2

A/Intons: 120/2; 169/1

C/Keywords: DNA binding; transcription factor

Query Match 99.7%; Score 2033; DB 2; Length 375;

Best Local Similarity 99.7%; Pred. No. 6e-146;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEMGNSGPGHGPQAGSGGSTMSSSFSGIMFGCKTYFDDGGSGSSSGGRNRRV 60
Db 1 MEMGNSGPGHGPQAGSGGSTMSSSFSGIMFGCKTYFDDGGSGSSSGGRNRRV 60

Qy 61 RGGSGGSGQIPRCVGECCGMDLTNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSR 120
 |||||
 Db 61 RGGGSGGQIPRCVGECCGMDLTNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSR 120
 Qy 121 FHOLEPFLERKSCRRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFL 180
 |||||
 Db 121 FHOLEPFLERKSCRRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFL 180
 Qy 181 GNOEIGWSSRLDTRVMRPPVSSPMQINPMNVPSQSGVGGRTSFSSPEIMDKLESY 240
 |||||
 Db 181 GNOEIGWSSRLDTRVMRPPVSSPMQINPMNVPSQSGVGGRTSFSSPEIMDKLESY 240
 Qy 241 KGIGDNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
 |||||
 Db 241 KGIGDNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
 Qy 301 OYLNPPWFKNDNDMSPLVNLGRYTEPDNCQISSGTAMGEFELSDHHOSRQYMEDN 360
 |||||
 Db 301 OYLNPPWFKNDNDMSPLVNLGRYTEPDNCQISSGTAMGEFELSDHHOSRQYMEDN 360
 Qy 361 TRAYDSSSHHTWMSL 375
 |||||
 Db 361 TRAYDSSSHHTWMSL 375

RESULT 2.

T52593

squamosa promoter binding protein homolog 9 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000

C:Accession: T52593

R:Cardon, G.H.; Hohmann, S.; Nettesheim, K.; Saedler, H.; Huijser, P.

Plant J. 12, 367-377, 1997

A:Title: Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a novel gene

A:Reference number: Z24029; PMID:9301089; PMID:9301089

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-373 <CAR>

A:Cross-references: EMBL:AJ011639; PIDN:CAB56591.1

A:Experimental source: cultivar Landsberg erecta; inflorescence

C:Genetics:

A:Gene: spl3

A:Map position:

C:Keywords: DNA binding; transcription factor

Query Match 95.9%; Score 1956; DB 2; Length 373;

Best Local Similarity 96.1%; Pred. No. 3.8e-140; Indels 14; Gaps 2;

Matches 366; Conservative 0; Mismatches 1; Indels 14; Gaps 2;

Qy 1 MEMGNSGPHGHPQQAESGSSSTESSFSGGLMFGOKIYFEDGGGSGSSSGGRSNRRV 60
 |||||
 Db 1 MEMGNSGPHGHPQQAESGSSSTESSFSGGLMFGOKIYFEDGGGSGSSSGGRSNRRV 60
 Qy 61 RGGGSGGSGQIPRCVGECCGMDLTNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSR 120
 |||||
 Db 61 RGGGSGGSGQIPRCVGECCGMDLTNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSR 120
 Qy 121 FHOLEPFLERKSCRRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFL 180
 |||||
 Db 121 FHOLEPFLERKSCRRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFL 180
 Qy 181 GNOEIGWSSRLDTRVMRPPVSSPMQINPMNVPSQSGVGGRTSFSSPEIMDKLESY 240
 |||||
 Db 181 GNOEIGWSSRLDTRVMRPPVSSPMQINPMNVPSQSGVGGRTSFSSPEIMDKLESY 240
 Qy 241 KGIGDNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 294
 |||||
 Db 241 KGIGDNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
 Qy 301 OYLNPPWFKNDNDMSPLVNLGRYTEPDNCQISSGTAMGEFELSDHHOSRQYMEDN 354
 |||||
 Db 301 OYLNPPWFKNDNDMSPLVNLGRYTEPDNCQISSGTAMGEFELSDHHOSRQYMEDN 354

Qy 355 YMEDENTRAYDSSSHHTWMSL 375
 |||||
 Db 355 YMEDENTRAYDSSSHHTWMSL 373

RESULT 3

T46014

squamosa promoter-binding protein homolog - Arabidopsis thaliana

N:Alternate names: protein T10K17.130

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46014

R:Benes, V.; Wurnbach, E.; Drzonek, H.; Ansoerge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23019

A:Accession: T46014

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-354 <BEN>

A:Cross-references: EMBL:AL132977

A:Experimental source: cultivar Columbia; BAC clone T10K17

C:Genetics:

A:Map position: 3

A:Introns: 105/2; 153/1

A:Note: T10K17.130

Query Match 42.3%; Score 863.5; DB 2; Length 354;

Best Local Similarity 52.7%; Pred. No. 9.3e-58; Indels 65; Gaps 17;

Matches 204; Conservative 3; Mismatches 86; Indels 65; Gaps 17;

Qy 14 GQAESGG-SSTESSFSGGLMFGOKIYFEDGGGSGSSSGGRSNRRVGGGSGGQIP 72

|||||

Db 8 GQAESGSSSTESSSLGGLRFGQKIYFEDG-----SGSRKSNRV--NTVKSSTTA 57

Qy 73 RCQVGGCMTDITNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSRFHOLESFDEKR 132

|||||

Db 58 RCQVGGCMTDITNAKGYSHRRVCGVHSKTPKVTAGIEGRFCQCCSRFHOLESFDEKR 117

Qy 133 SCRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFLGNOEIMPSERT 192

|||||

Db 118 SCRRLAGHNERRRKQPASLSTLARYGRIASLYLENGDAKNGSFLGNOEIMPSERT 175

Qy 193 LDTVMRRPVPSSPMQINP-----NNVPSQSGVGGRTSFSS-PEIMDKLESYKIG 244

|||||

Db 176 ---VMQRP---GPMQINPVARETHPHMNVLSHGS-----SFTTCPEMINNST- 217

Qy 245 DSNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 293

|||||

Db 218 DSNCALSLISNPHQPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 271

Qy 294 -PPAPSGHQYNPMPV-----KNDNDMSPLVNLGRYTEPDNCQISSGTAMGEFELSDH 348

|||||

Db 212 QPPISTHOQVLSQTWELVAGEKSHYMSPV---SQISEPADFOISNGTIMGFEELY-LH 327

Qy 349 HQSRQYMEDENTRAYDSSSHHTWMSL 375

|||||

Db 328 QQVLKQVMEPENTRAYDSSPHFWMSL 354

RESULT 4

T52297

squamosa promoter binding protein-homolog 5 (imported) - garden snapdragon (fragment)

C:Species: Antirrhinum majus (garden snapdragon)

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

C:Accession: T52297

R:Cardon, G.H.; Hohmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.

Gene 237, 91-104, 1999

A:Title: Molecular characterisation of the Arabidopsis SBP-box genes.

A:Reference number: Z25236; PMID:99453765; PMID:10524240

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-419 <CAR>
A:Cross-references: EMBL:AJ011626; PIDN:CAB56578.1
A:Experimental source: cultivar Columbia; inflorescence
C:Genetics:
A:Gene: sp12
A:Map position: 5
C:Keywords: DNA binding; transcription factor

Query Match 19.2%; Score 392; DB 2; Length 419;
Best Local Similarity 31.5%; Pred. No. 8.4e-21;
Matches 116; Conservative 49; Mismatches 111; Indels 92; Gaps 16;

Qy 13 PQQAESG---GSTSTSSPSFG---GLMFGKITYED-----GGGSG-----SSSG 53
Db 94 PEFKAGIDTSPSLSPSSGDPVLGKIGKRTYEDFEVENAGLGLPYTLASSVSP 153
Qy 54 GSNRRVRGGSGGSGQIPRCVGGCMTLNAGYSHRVGVHSTKPYTVAGIEOR 113
Db 154 VKSKSI-----PQRLQTHCQVEGNCNLDLSAKDYHRKGRICENHSKPKVVGVER 208
Qy 114 FQOQSRFHQLPEPDLKSCRRRLAGHNERRRKQPA-----SLSTLARYGRIAPS 166
Db 209 FQOQSRFHQLSEPEKRSRRRLSDHARRKRPRTYDGKQVDPVWNRFAIHR 268
Qy 167 LYENDGAGNGSFLNGOIGMPSRTLDTRY-MRRPVSS--PSMOINPMNVFSGSGVGG 223
Db 269 -----SBEKTIWPSKXVPERVLMPOPAKIEIDTEHNRGLDPTKTRK 314
Qy 224 RTSFSSPEIMDTKLESYKIG-DSNCALSLSPHOPHDNNNNNNNNNNNNNNNNNNNN 282
Db 315 AELFKEKEV---TISHWGASQDLGALSLSL-----NSTTW-VSSS 352
Qy 263 FCPMTVTMAQPPA---PSQHQYLNPPWFKNDNDMSVYMLGRTYEDNQISSGTAM 339
Db 353 DQPRFTLDHHSNMQPVAR-----SAAQLNSVSGWDDPPAVEGPTAL 399
Qy 340 -----GEF 342
Db 400 HRNGVQGF 407

RESULT 8

152592
squamosa-promoter binding protein 6 [imported] - Arabidopsis thaliana
N:Alternate names: transcription factor sp16
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52592
R:Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.
Gene 237, 91-104, 1999
A:Title: Molecular characterization of the Arabidopsis SBP-box genes.
A:Reference number: Z25236; MUID:99453765; PMID:10524240
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T52592
A:Molecule type: mRNA
A:Residues: 1-405 <CAR>
A:Cross-references: EMBL:AJ011643; PIDN:CAB56595.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: sp16
A:Map position: 2
C:Keywords: DNA binding; transcription factor

Query Match 18.4%; Score 374.5; DB 2; Length 405;
Best Local Similarity 32.4%; Pred. No. 8.4e-21;
Matches 122; Conservative 38; Mismatches 139; Indels 77; Gaps 14;

Qy 15 QAESGSGSTSSPSFGMLFGQKIYF-----DGGGSGSSSSSGSRNRVRVGGSGGSG 69
Db 62 BEEDENISSSKSFSSQEL-NRIDFKLSFLDLGNDDDTSSRGPALEPKSRASNLCS 119

Qy 70 QIPRCVGGCMTLNAGYSHRVGVHSTKPYTVAGIEORFQOQSRFHQLPEFDL 129
Db 120 QNPCLQYVGCSDLSKSDYKRRHVRCEBAHSKTSVIVNGLEQGFQOQSRFHFLSEFDD 179
Qy 130 EKRCRRRLAGHNERRRKQPAASLVASRYGRVAPLYENGDAQNGMSFLGNQEIOWPS 189
Db 180 GKRCRRRLAGHNERRRK-PAFYFLPKRH-----KLRTSQDVANKFLSNSLVLP 232
Qy 190 S-----RTLDTRYMR--PEVS--SPSMOINPMNVFSGSGVGGRTSPSPIMDTKL 237
Db 233 SFPSSLYRVIVDEDDHTRSLVSKDEFTGCMFPTN--EQNS--SRITYSKPAIYSTEV 287
Qy 238 ESYKIGD---SNCALSLSPHOPHDNNNNN-----NNNNNNNNNNNNNNNNNNNN 284
Db 288 SSIMDLHETASRSTRALSLISAQOHLISKFPPTTESITQPNQNLNHSST----- 339
Qy 285 PMYTMQPPAPQHQYLNPPWFKNDNDMSVYMLGRTYEDNQISSGTAMGEFL 344
Db 340 -----DYHQWEOPLWIDPKTNSAG-----SSCKGKGTSTVDLLQL 376
Qy 345 SDH--HHOSRQYMED 358
Db 377 SSHLQRIEQCRNNTGD 392

RESULT 9

152596
squamosa promoter binding protein homolog 10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52596
R:Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.
Gene 237, 91-104, 1999
A:Title: Molecular characterization of the Arabidopsis SBP-box genes.
A:Reference number: Z25236; MUID:99453765; PMID:10524240
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T52596
A:Molecule type: mRNA
A:Residues: 1-396 <CAR>
A:Cross-references: EMBL:AJ011637; PIDN:CAB56589.1
A:Experimental source: cultivar Columbia; inflorescence
C:Genetics:
A:Gene: sp110
C:Keywords: DNA binding; transcription factor

Query Match 17.5%; Score 356; DB 2; Length 396;
Best Local Similarity 29.4%; Pred. No. 2e-19;
Matches 103; Conservative 40; Mismatches 97; Indels 110; Gaps 11;

Qy 3 MGSNSGPHG-----PGQA-ESGSGSTSSPSFGIMFGQKIYFDDGGGSGSS 51
Db 90 LASQSPDSSNIDPLQVXPSTALEVPVIAABEDLC--LKGKRTYSEBFGMRNNNDL 146
Qy 52 SGGSN-----RRVGGSGGSGQIPRCVGGCMTLNAGYSHRVGVHSTKPY 104
Db 147 SAVEMNLTPSVVARKTKKSCGQGMQVPRQIDCELDLSSKDYHKKHRCETHSKCPK 206
Qy 105 VTVAGIEORFQOQSRFHQLPEPDLKSCRRRLAGHNERRRKQPAASLVASRYGRIA 164
Db 207 VVVGLERRFQOQSRFHAVSEPEKRSCKRSLSHNARRKQ---GVFLNSERV 262
Qy 165 PSLYENDGAGNGSFLNGOIGMPSRTLDTRYVRRPVSSPSMOINPMNVF----- 216
Db 263 -----DRQHTSMWN-----GLSLNTRSEKXTWGTYTEKPTQWESSGTTLSFOR 308
Qy 217 -----QGSVGGGRTSFSBPIMDTKLESYKIG-----D 245
Db 309 GNGSEDQLFTGSTLSFAFQTSGGFSAKSNIQLPD-----KGVGCSGGGLHESHD 359
Qy 246 SNCALSLSPHOPHDNN 295
Db 360 FYSALSLST-----TSDSQGIKHTPVABPP 386

RESULT 10

B86399

Protein F17L21.14 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: B86399

R/Theologian: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

anzen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: B86399

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-389 <STO>

A/Cross-references: GB:AE005172; NID:99802531; PIDN:AAF9733.1; GSPDB:GN00141

C/Genetics:

A:Gene: F17L21.14

A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

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A:Map position: 1

A:Map position: 1

A:Map position: 1

C/Genetics:

A:Gene: sp11

A:Map position: 1

A:Map position: 1

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A:Map position: 1

A:Map position: 1

A:Map position: 1

A:Map position: 1

C/Genetics:

A:Gene: sp11

A:Map position: 1

A:Map position: 1

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A:Gene: sp11

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562361
 Squamosa-promoter binding protein 2 - garden snapdragon
 C:Species: Antirrhinum majus (garden snapdragon)
 C:Date: 23-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: S62361
 R:Klein, J., Seedler, H., Huijser, P.
 Mol. Gen. Genet. 250, 7-16, 1996
 A:Title: A new family of DNA binding proteins includes putative transcriptional regulators
 A:Reference number: S62360; MUID:96158840; PMID:8569690
 A:Accession: S62361
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-171 <KLE>
 A:Cross-references: EMBL:X92079; NID:G1183863; PIDN:CAA63061.1; PID:G1183864

Query Match 16.2%; Score 330; DB 2; Length 171;
 Best Local Similarity 43.4%; Pred. No. 7.3e-18;
 Matches 65; Conservative 5; Mismatches 28; Indels 4; Gaps 2;

Qy 46 GSGSSSSGGRNRRVGGSGGSGQIPRCQVEGCGMDLTNAAGYYSRRHVCVHSTKTPKV 105
 Db 61 GGG---SSGKSEKKTATASGCVAAQ-PCCLVENCGADLNCKKYYQHRVCEVHAKAPV 116
 106 TVAGIEGRFCQCCSRFHQLPEFDLEKRSRRRLAGHNERRRK 147
 117 SVEGLMORFCQCCSRFHDLSEFDQTKRSRRRLAGHNERRRK 158

RESULT 14
 T52607
 Squamosa promoter binding protein 5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
 C:Accession: T52607
 R:Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Seedler, H.; Huijser, P.
 Gene 237, 91-104, 1999
 A:Title: Molecular characterisation of the Arabidopsis SBP-box genes.
 A:Reference number: Z25236; MUID:99453765; PMID:10524240
 A:Accession: T52607
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-181 <CAR>
 A:Cross-references: EMBL:AJ011610; PIDN:CAB56572.1
 A:Experimental source: cultivar Landsberg erecta; Inflorescence
 C:Genetics:
 A:Gene: sp15
 A:Map position: 3
 C:Keywords: DNA binding; transcription factor

Query Match 16.2%; Score 330; DB 2; Length 181;
 Best Local Similarity 43.4%; Pred. No. 7.3e-18;
 Matches 75; Conservative 22; Mismatches 42; Indels 34; Gaps 7;

Qy 45 GSGSSSSGGRNRR-----RVGGSGSGSGQIPR--COVEGCGMDLTNAAGYYSRRHVC 96
 Db 29 GMDGDEEDGDDCKKKVMERVVG--PSTIDVPSRLCQVDRCTVNLTEAKQYRRHRVC 85
 Qy 97 GVHSTPKTVAGIGIRFCQCCSRFHQLPEFDLEKRSRRRLAGHNERRRKQOPASLSVL 156
 Db 86 EVHADAQAATVAVGVRFCQCCSRFHQLPEFDLEKRSRRRLAGHNERRRK-----IS 138
 Qy 157 ASRYGRIPASLYENGAGMNGSFLGNOEIGWPSRRLDTRVMNR--PVSSPSWQ 208
 Db 139 GDSFGE-----GSGRGRFSGQLIQTE-----RNRVDRKLPMTNSSPK 176

RESULT 15
 H96793
 unknown protein FLAG6.18 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96793
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huitzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96793
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1020 <STO>
 A:Cross-references: GB:AE005173; NID:96642682; PIDN:AAF20262.1; GSPDB:GN00141
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 A:Gene: FLAG6.18
 A:Map position: 1

Query Match 16.1%; Score 328.5; DB 2; Length 1020;
 Best Local Similarity 29.7%; Pred. No. 7.4e-17;
 Matches 105; Conservative 36; Mismatches 104; Indels 109; Gaps 13;

Qy 55 RSNRRV-----GGSGSGSGQIPRCQVEGCGMDLTNAAGYYSRRHVCVHSTKTPKVAGI 110
 Db 91 RSKKVRSGSPSGSGGGGNYPKQVNDCKEDLSIADYHRRHVCVHSTKTPKVAGI 150
 Qy 111 EORFCQCCSRFHQLPEFDLEKRSRRRLAGHNERRRKQP----- 150
 Db 151 MORFCQCCSRFHLSFDEGRKSCRRLDGHNRRTKQPPALINSQVVALENRNTSNT 210
 Qy 151 -----ASISVLASRYGRIPASLYENGAGMNGSFLGNOEIGWPSRRLDTRVMRPPVSSP 205
 Db 211 NMDVALLTALVCAQGR-----NEATTNGS-----PGVPOREOL-LQILNKIKALP 255
 Qy 206 SWQINPMNVFQSGVGGGRTSFSSPEIMDTLSEYKIGGNSCALSLSNPHOPHDNNN 265
 Db 256 L-----PNNLTS-----KL-----NNIGILARKNPEQSPNMPQ 284
 Qy 266 NNNNNNNNNNTW-----RASSGFGMTVTMAQPPAPSOHQYLPVWFVKNDNDMSPVLN 321
 Db 285 NSMNGASSPSTMDLALSLASLG-----SSAPEIAFLSGGFGNGESNDR----- 331
 Qy 332 LGRYTEPDNCOISSGTAM-----GEFLSDHHHQSRRQWEDENTRA 363
 Db 332 --KLTSDDH--SATTSLKKTLEFPFGGERTSTNHSQYSDSRGQDTRS 380

Search completed: April 10, 2003, 13:54:35
 Job time : 23 secs

PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERRINDUNGEN VERW GES MBH.
XX
XX Schmidt EDL, De Vries SC, Hecht VFG;
XX WPI, 2000-350753/30.
DR N-PSDB; AAD00300.
XX
XX
PT Increasing vegetative production of a new plant generation through
PT apomixis, comprising transgenically expressing a gene encoding a
PT protein acting in the signal transduction cascade triggered by the
PT Somatic Embryogenesis Receptor Kinase
XX
XX Claim 4, Page 26-27, 45P; English.
XX
XX The patent discloses a method for increasing vegetative reproduction of
XX plants through seeds called apomixis, by transgenic expression of a gene
XX encoding a protein acting in the signal transduction cascade, triggered
XX by Somatic Embryogenesis Receptor Kinase (SERK). The protein physically
XX interacts with SERK, that is involved in the formation of extraneous
XX embryos from sporophytic cells, which can result in apomictic seeds.
XX This method is useful for increasing vegetative reproduction in vivo
XX through seeds or in vitro by somatic embryogenesis.
XX The present amino acid sequence is the SERK-interacting protein #1,
XX isolated from clone 3A35. It is obtained by RT-PCR amplification of
XX early stage Arabidopsis salique RNA. It is a member of the family of
XX Squamosa-promoter Binding Protein (SBP) transcription factors. SERK
XX transphosphorylates cytoplasmic SBP-transcription factors, after binding
XX of 13and, followed by nuclear translocation of the factors and binding
XX to specific regulatory DNA target sites on the genome.
XX
XX Sequence 375 AA;
SQ
Query Match 100.0%; Score 2040; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. NO. 3.9e-176;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEMGNSGPGHGPQAESEGSSTESSSFGGLMFGQKTYFEDGGGSGSSSGRNSRRV 60
Db 1 MEMGNSGPGHGPQAESEGSSTESSSFGGLMFGQKTYFEDGGGSGSSSGRNSRRV 60
QY 61 RGGSGSGGQIIPRCVGGCGMDLTNAKGYSHRVCGVSKTPKTVAGIEORFCQCSR 120
Db 61 RGGSGSGGQIIPRCVGGCGMDLTNAKGYSHRVCGVSKTPKTVAGIEORFCQCSR 120
QY 121 FHOPEPFLERKSCRRRLAGHERRRRPPASLVLASRYGRIASLYENGAGNNGSFL 180
Db 121 FHOPEPFLERKSCRRRLAGHERRRRPPASLVLASRYGRIASLYENGAGNNGSFL 180
QY 181 GNOEIGWSSRLTDRVMRRPVSSPSWQINPMNVFSQSGVGGRTSFSSPEIMDKLSBY 240
Db 181 GNOEIGWSSRLTDRVMRRPVSSPSWQINPMNVFSQSGVGGRTSFSSPEIMDKLSBY 240
QY 241 KGIGDNCALSLNSPHOPHDNNNNNNNNNNNTWRASGFGPMYTTMAOPPAPOH 300
Db 241 KGIGDNCALSLNSPHOPHDNNNNNNNNNNNTWRASGFGPMYTTMAOPPAPOH 300
QY 301 OYLNPPWPKDNDNMSPTLNGRYTEPDNCOISGTAMGEFELSDHHOSROYMEDN 360
Db 301 OYLNPPWPKDNDNMSPTLNGRYTEPDNCOISGTAMGEFELSDHHOSROYMEDN 360
QY 361 TRAYDSSSHHTWMSL 375
Db 361 TRAYDSSSHHTWMSL 375
RESULT 2
AAG31717
ID AAG31717 standard; Protein; 375 AA.
XX AAG31717;
AC AAG31717;
XX
DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 38136.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
XX Arabidopsis thaliana.
EN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
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XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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XX 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
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XX 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
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XX 17-JUN-1999; 99US-0139453.
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PR 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
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PR 18-JUN-1999; 99US-0139462.
XX 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
XX 18-JUN-1999; 99US-0139763.

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PR	24-JUN-1999;	99US-0140354.
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PR	26-JUN-1999;	99US-0140823.
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Qy 301 QYLNPPWVFKDNDNMSPYLNIGRYTEPDNCQISSGTAMGEFELSDHHQSRQYMEDEN 360
Db 301 QYLNPPWVFKDNDNMSPYLNIGRYTEPDNCQISSGTAMGEFELSDHHQSRQYMEDEN 360
Qy 361 TRAYSSSSHTWTWSL 375
Db 361 TRAYSSSSHTWTWSL 375

RESULT 3
AAG31718
ID AAG31718 standard; Protein; 373 AA.
XX
AC AAG31718;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38137.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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RESULT 5
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AC AA616707;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 17456.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 19-JUL-1999; 99US-0144325.
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PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
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PR	28-OCT-1999;	99US-0161982.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

	Query Match	98.1%	Score 2000.5	DB 21	Length 376
	Beat Local Similarity	98.7%	Pred. No. 1.5e-172		
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Qy	3	MGNSGPGHGPQQAESGSGSTSSSPSGGIMFGQKIYFEDGGGGSGSSSGGRSNRRVG	62		
Db	1	MGNSGPGHGPQQAESGSGSTSSSPSGGIMFGQKIYFEDGGGGSGSSSGGRSNRRVG	60		
Qy	63	GGSGSQGQIPRCQVEGGGMDLTAKGYSHRVCGVHSKTPKTVAGIEGRFCQGRFH	122		
Db	61	GGSGSQGQIPRCQVEGGGMDLTAKGYSHRVCGVHSKTPKTVAGIEGRFCQGRFH	120		
Qy	123	QLPEFDEKESCRRLRAGHNERRRKQPAASLVASHYGRVIAPELVENGDAGNNGSFLGN	182		
Db	121	QLPEFDEKESCRRLRAGHNERRRKQPAASLVASHYGRVIAPELVENGDAGNNGSFLGN	180		
Qy	183	QETMPSPSRLDRTVWRPVSFSPWQINPMNVNSQGSVGGGRFSFSPSPPELMDTKLESYNG	242		
Db	181	QETMPSPSRLDRTVWRPVSFSPWQINPMNVNSQGSVGGGRFSFSPPELMDTKLESYNG	240		
Qy	243	IGDSNICALSLISNPHQPHD--NNNNNNNNNNNNNTWRASSGFGEPTVTMAQPPAPSQ	299		
Db	241	IGDSNICALSLISNPHQPHDNNNNNNNNNNNNNNNNNTWRASSGFGEPTVTMAQPPAPSQ	300		
Qy	300	HOYINPWPVEKNDNDMSPYVLNIGRYTEPNCOISSGTAMGEFELSDHHQSRQYMEDE	359		
Db	301	HOYINPWPVEKNDNDMSPYVLNIGRYTEPNCOISSGTAMGEFELSDHHQSRQYMEDE	360		
Qy	360	NTRAYDSSSHHTWMSL 375			
Db	361	NTRAYDSSSHHTWMSL 376			
RESULT 6					
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ID	AAG31719	standard; Protein; 343 AA.			
XX	AAG31719;				
XX	17-OCT-2000	(first entry)			
XX	Archidopsis thaliana	protein fragment SEQ ID NO: 38138.			
XX	Protein identification:	signal transduction pathway; metabolic pathway;			
XX	hybridisation assay;	genetic mapping; gene expression control; promoter;			

KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
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Query Match 91.5%; Score 1866; DB 21; Length 343;
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DB 1 MFGOKIYFEDGGGSGSSSGSRNRVYGGGSGGQI PRQVYEGCGMDLTNAKYYSR 60
QY 93 HRVCGVHSHKTPKVTYAGIEORFCQCCSRFHQIPEPDLKRSRRRLAGHNERRRKPOAS 152
DB 61 HRVCGVHSHKTPKVTYAGIEORFCQCCSRFHQIPEPDLKRSRRRLAGHNERRRKPOAS 120
QY 153 LSVLASRYGRITAPSLYXMGDAGMNSFLGNQBIGPSSRTLTTRVMRRPVSSPQIINPM 212
DB 121 LSVLASRYGRITAPSLYXMGDAGMNSFLGNQBIGPSSRTLTTRVMRRPVSSPQIINPM 180
QY 213 NVFSQGSYGGGRTFSFSPIMDTKLESYKIGICDSNCALSLSNPQHPDNNNNNNNNNN 272
DB 181 NVFSQGSYGGGRTFSFSPIMDTKLESYKIGICDSNCALSLSNPQHPDNNNNNNNNNN 240
QY 273 NNNWTWRASSGFGCPMTVTMAQPPAPDSOHQYLPVWFKQNDNDMSPVNLGATYTPDNCQ 332
DB 241 NNNWTWRASSGFGCPMTVTMAQPPAPDSOHQYLPVWFKQNDNDMSPVNLGATYTPDNCQ 300
QY 333 ISSGTAMGEFELSDHHQSRROYMBEDENTRAYDSSSHHTNWSL 375
DB 301 ISSGTAMGEFELSDHHQSRROYMBEDENTRAYDSSSHHTNWSL 343

RESULT 7
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ID AAG16708 standard; Protein; 346 AA.
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AC AAG16708;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17457.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 29-MAR-1999; 99US-0126264.
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PR 23-APR-1999; 99US-0130891.
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PR 04-JUN-1999; 99US-0137502.
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Query Match 90.4%; Score 1843.5; DB 21; Length 346;
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 Matches 341; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

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QY 33 MFGOKTYFEDGGGSSSSGGRSNRRVRGGSGGSGOIPRCQVEGGMGLTNAKGYSR 92
Db 1 MFGOKTYFEDGGGSSSSGGRSNRRVRGGSGGSGOIPRCQVEGGMGLTNAKGYISR 60
QY 93 HRVGVHAKTKPTVTAGIEORFCQOCRSFHOPEFPLEKRSRRRLAGHNERRRKQOPAS 152
Db 61 HRVGVHAKTKPTVTAGIEORFCQOCRSFHOPEFPLEKRSRRRLAGHNERRRKQOPAS 120
QY 153 LSVLASRYGRIAPSLYENGAGANGSFLGNQOETGWPSSRLTLDRVWRPVPVSSSQINPM 212
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Qy 213 NVFSGSVGGRTSFSSEINDTKLESYKGI GDSNCALSLSPHQPHD---NNNNNNNN 269
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Qy 270 NNNNNNTWRASSGCGPMTVTAQPPAPSOHQYLNPPVFKDNDNDMSPVNLGRYTEPD 329
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RESULT 8
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ID AACG22917 standard; Protein: 350 AA.
AC MAG22917;
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26028.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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Query Match 42.3%; Score 863.5; DB 21; Length 354;
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Matches 204; Conservative 32; Mismatches 86; Indels 65; Gaps 17;

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DB 118 SCRRRLAGHNERRRKPPQPTT-ALFTSHYSRIAPSLYENPNAMKSVLGD-PTAMSTARS 175
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ID AAG22918 standard; Protein; 289 AA.

AC AAG22918;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 26029.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KM homeodomain zipper; LIM domain; AP2; ERBBs; zinc finger domain;
XX type 2 Cys2His2; CCAAT box element; MYB.
OS Eucalyptus grandis.
XX MO200053724-A2.
XX PN 14-SEP-2000.
XX PD 09-MAR-2000; 2000MO-US06112.
XX PF 11-MAR-1999; 99US-0266513.
XX PR 18-AUG-1999; 99US-0149485.
XX PS (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Wood M, McGrath A, Shenk MA, Glenn M,
XX WPI; 2000-579369/54.
XX DR New isolated polynucleotide encoding a plant transcription factor for
XX PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
XX PT having modified gene expression or modified activity of a polypeptide
XX -
XX PS Claim 8; Page 612; 747pp; English.
XX CC The present invention relates to novel plant transcription factors from
XX CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
XX CC transcription factor. The transcription factor may be used to produce a
XX CC plant having modified gene expression such as a woody plant e.g. a
XX CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
XX CC to modify the activity of a polypeptide in a plant. The transcription
XX CC factors of the present invention are members from the following families
XX CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
XX CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
XX CC zipper, LIM domain, AP2 and ERBBs, zinc finger domains of type 2
XX CC Cys2His2, CCAAT box elements and MYB.
XX SQ Sequence 230 AA;
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Query Match 25.2%; Score 514.5; DB 21; Length 230;
Best Local Similarity 57.1%; Pred. No. 2,3e-38;
Matches 112; Conservative 15; Mismatches 40; Indels 29; Gaps 6;
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Db 64 PGSGTPEPKKVASAGGGCGAIOGQPPRCOVGCGRVLSAKAYSHRKCGMHSKAT 123
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Db 124 VIVAGIEORFCQCGSRFQLEPFDEKRSRRRLAGHERRRKKPPGSL--LSRYGRIQ 181
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RESULT 12
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XX AAG12773;
XX AC AAG12773;
XX DT 17-OCT-2000 (first entry)
XX XX Arabidopsis thaliana protein fragment SEQ ID NO: 12015.

XX XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX PN 06-SEP-2000.
XX PD 25-FEB-2000; 2000EP-0301439.
XX PF 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
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PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161922.
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PR 29-OCT-1999; 99US-0162142.
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Best Local Similarity 31.3%; Pred. No. 9e-28;
Matches 121; Conservative 50; Mismatches 108; Indels 108; Gaps 17;
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D6 65 PGEPAKGDITPTLELSFGSDPVLGLTKRITYEDFEWEYENAKGLGLPVSLASSVSP 124
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QY 114 FCQCCSRPHOLPEPDLERKSGRRRLAGHNERRRKQPA-----SLSVLSRYGRIAPS 166
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D6 240 SEF-----KFL-----MPSKRPVSRVL---MPQPAKEISNKLFTESRGLDLP 282
QY 224 RTSFSSPEIMDTK--LESYKIG-DSNCAISLSNPHQPHDNNNNNNNNNTTARA 279
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QY 280 SSGRCPTVTMAQPPAPASQOYLNPWFVKDNDMSVPLN-----LGRYTEPDNC 331
D6 324 SSSDQPRRTLDHNP-----SSNLDQVARRSAQSLSSVGYWQDPDP 365
QY 332 QISSGTAMGEFELSDHHQSRQYMED 358
D6 366 AVEGFTAL-----HNGAQGFEN 384
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AC AAG12772;
XX 17-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX OS
XX EP1033405-A2.
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XX PD
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 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 19.7%; Score 401; DB 21; Length 425;
 Best Local Similarity 31.3%; Pred. No. 1e-27;
 Matches 121; Conservative 50; Mismatches 108; Indels 108; Gaps 17;

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 QY 167 LYENGAGMNGSFLGNQELGMPSSRTLDTFVMRRPVSSPSWQJNPMNVFSQSGVG---G 223
 DB 272 SEB-----KFL-----WPSKVPVSRVL---MPQAKTEISNLTFTFHSRFGILDP 314
 QY 224 RTFSSEPIMDTK---LESYKIG-DSNCALSLISNPHQHDNNNNNNNNNNNTWRA 279
 DB 315 KTKSARAELEFSKEKVTITSHMGASODLDGALSLIS-----NSTTW-V 355
 QY 280 SSGFGPMTVMAOPPAPOHQYLNPPWVFPKDNNDMSPVLN-----LGRYTEPDNC 331
 DB 356 SSSDQPRRFTLIDHP-----SSNIQPVANSAAQLSVSGYMQDPDP 397
 QY 332 QISSGTAMGEFELSDHSHQSRROYMED 358
 DB 398 AVEGPFTAL-----HRNAGAGQENEN 416

Search completed: April 10, 2003, 13:53:04
 Job time : 39 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:52:29 ; Search time 14 Seconds

(without alignments)
788.114 Million cell updates/sec

Title: US-09-839-185-2

Perfect score: 2040
Sequence: 1 MEMGNSGPHGPGQAESEGC.....MEDENTRAYDSSHTTWSL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	152	7.5	1584	US-09-457-040B-27	Sequence 27, Appl
2	115.5	5.7	591	US-08-965-903B-2	Sequence 2, Appl
3	105	5.1	1234	US-08-317-310A-15	Sequence 15, Appl
4	105	5.1	1234	PCT-US95-13041-15	Sequence 15, Appl
5	105	5.1	2391	US-08-446-855A-2	Sequence 2, Appl
6	105	5.1	2391	US-09-150-741-2	Sequence 2, Appl
7	104	5.1	246	US-09-451-117-2	Sequence 2, Appl
8	102	5.0	888	US-08-861-464-6	Sequence 6, Appl
9	102	5.0	888	US-08-396-001-6	Sequence 6, Appl
10	102	5.0	888	US-09-323-433A-6	Sequence 6, Appl
11	100.5	4.9	432	US-09-118-319-2	Sequence 2, Appl
12	100.5	4.9	2938	PCT-US94-00198-3	Sequence 3, Appl
13	100	4.9	286	US-09-384-162-6	Sequence 6, Appl
14	100	4.9	424	US-09-120-817-2	Sequence 2, Appl
15	100	4.9	732	US-08-914-999-8	Sequence 8, Appl
16	99.5	4.9	542	US-07-814-964-13	Sequence 13, Appl
17	99.5	4.9	542	US-08-258-442-13	Sequence 13, Appl
18	99.5	4.9	542	US-08-328-809-8	Sequence 8, Appl
19	99.5	4.9	542	PCT-US92-11107-13	Sequence 13, Appl
20	98.5	4.8	444	US-07-881-075-3	Sequence 3, Appl
21	98.5	4.8	444	US-08-120-827-3	Sequence 3, Appl
22	98.5	4.8	444	US-08-478-675-3	Sequence 3, Appl
23	98.5	4.8	571	US-09-134-001C-3865	Sequence 3865, Ap
24	98.5	4.8	2414	US-08-227-536-2	Sequence 2, Appl
25	98.5	4.8	2414	PCT-US95-04682-2	Sequence 2, Appl
26	97	4.8	127	US-08-789-333F-43	Sequence 43, Appl
27	97	4.8	127	US-08-787-738B-43	Sequence 43, Appl

28	96	4.7	596	US-09-752-165-2	Sequence 2, Appl
29	96	4.7	655	US-08-857-076-57	Sequence 57, Appl
30	95.5	4.7	447	US-09-916-109-5	Sequence 5, Appl
31	95.5	4.7	483	US-09-916-109-4	Sequence 4, Appl
32	95	4.7	674	US-08-317-522A-3	Sequence 3, Appl
33	95	4.7	674	US-08-439-818A-3	Sequence 3, Appl
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37	95	4.7	674	US-08-808-599A-3	Sequence 3, Appl
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45	94.5	4.6	666	US-09-528-784A-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
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Sequence 27, Application US/09457040B
Patent No. 6387641
GENERAL INFORMATION:
APPLICANT: Bellon, Steve
TITLE OR INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98-14
CURRENT APPLICATION NUMBER: US/09/457, 040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1584
TYPE: PRT
ORGANISM: DICTD - Dictyostelium Discoideum
US-09-457-040B-27

Query Match 7.5%; Score 152; DB 4; Length 1584;
Best Local Similarity 20.3%; Pred. No. 1.8e-05;
Matches 97; Conservative 54; Mismatches 153; Indels 174; Gaps 19;

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DB	270	DKGQL-----SIGLANLEY-----PTFY-----	288
QY	185	IGW-PSS---RTLDTRVWRVRVSSPSQINP-----NMVFGSGVGGRTSFSSPEI	232
DB	289	VGMNFRSGYHNDQKFR-----WKEPGVNEGSEYSGSYKKGDIIGGLSFTSKEI	341
QY	233	MDTLLESYKIGDNC-----AUSLSNPHQ-----	258
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QY	259	PHDNNNNNNNNNNNNNTWRASGSGFPVTVMAQPPAPSGQYVL-----NPPWFKNDN	314
DB	402	PNGNNNNNNNNNNNNNNIIGNGKITTTTSTSPSSINNEDISSNNNNNNNNNNNNNN	461

Qy 315 DMSFVNLGRYTEPNCOISGTMGEFELSDHHQSRQYMEDETRAYDSSSHHTN 372
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RESULT 2

US-08-965-903B-2
 ; Sequence 2, Application US/08965903B
 ; Patent No. 6060275
 ; GENERAL INFORMATION:
 ; APPLICANT: Hachon, Nit
 ; APPLICANT: Krasnow, Mark A.
 ; TITLE OF INVENTION: SPROUTY PROTEIN AND CODING
 ; TITLE OF INVENTION: SEQUENCE
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Denlinger & Associates
 ; STREET: 350 Cambridge Ave., Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/965, 903B
 ; FILING DATE: 07-NOV-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/030232
 ; FILING DATE: 07-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Petilchory, Joanne R
 ; REGISTRATION NUMBER: 42,995
 ; REFERENCE/DOCKET NUMBER: 8600-0177.30
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880
 ; TELEFAX: 650-324-0960
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 591 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-965-903B-2

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 Db 84 ASPPDDVDQIHLTLPLQRPSSLSRNSSTASSTTATGIVSGSGVSSSFTFTR----- 138
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 Qy 233 PPAPSQHOYLNPWFKNQNDMSFVNLGRYTEP-----DNCQISSGTAM-----GEF 342
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Qy 343 EISDH--HHSRRQYMEDETRAYDSSSHHTN 372
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RESULT 3

US-08-317-310A-15
 ; Sequence 15, Application US/08317310A
 ; Patent No. 5858701
 ; GENERAL INFORMATION:
 ; APPLICANT: WHITE, Morris F.
 ; APPLICANT: SUN, Xiao Jian
 ; APPLICANT: PIERCE, Jacalyn H.
 ; TITLE OF INVENTION: THE IRS FAMILY OF GENES
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/317,310A
 ; FILING DATE: 03-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Louis Myers
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: JDP-022
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-08-317-310A-15

Query Match 5.1%; Score 105; DB 2; Length 1234;
 Best Local Similarity 21.0%; Pred. No. 0.36;
 Matches 104; Conservative 57; Mismatches 176; Indels 158; Gaps 25;

Qy 1 MEMGNSGPGHQPQAEQSGSSTESSPSGGIMFQKITYPEDG----- 44
 Db 385 VLSSTSTSGHG-STSDCLFRRSSASVSGSPSDGFLSSDEYSGSPCDFSSPFSVTDP 443
 Qy 45 -----GSGSGS-----SSGGRSNNRVVGGSGGSGGQIQR 73
 Db 444 SLGHTPPARGEELSNVYICMGKGKASTLAEPNGHYILSRGGNGHRYIGAMIGTSPALPG 503
 Qy 74 COVECGMDLTNAKYRYRHRVCV-----HSTP-KTYVAGIEGRFCQCSR----- 121
 Db 504 DEAGAA-DLNR--FRKRTSAGTSPITISHQKTPSOSSVASIEEYTEMPPAAYPPGGG 560
 Qy 122 -----HQPEFDLEKSCRRRLAGHNERRRKQPPASLVLASRYGRIAPS 166
 Db 561 GGRLPCHSAFVPTHYSPEEGLEMHLERR-GGHH---RPTYSNLT- DDGYWMPF- 613
 Qy 167 LYENDAGMGNGSLNQRIGWPSRTLDTRYVRRFVSSPSWQIND-----YN 213
 Db 614 ----GVAIPVSNRKNGY-WPMS-----PKSVSAPOQIINIRHHPQKVDPNGYM 660
 Qy 214 VFSQGS-----VGGFTSPSSPEIMDKLESY-----KIGDSNC-ALSLSLNPHO----- 258

Db 661 MSPGSCSPDIGGSSSSSSISAAPSG-SSYCKPWTNGVGHHTHALPHAKPVESGGCK 719
 QY 259 --PHDNNNNNNNNNNNTWRASSGFGPMTVTWAQPPAPSOHQYLNPPVFKDNDNM 316
 Db 720 LLPCTGYMNMSPVGDSTSSPSECYGP-----EDQHKPVLSTYSLPSRFHGTORG 773
 QY 317 SPV-----LNLG-----RY--TEPDNCOISSGTAMG-----EFELSDHHQSR 353
 Db 774 EPEGARHOLRLSSSGRLRYTATAEDSSSTSDSLGGGCGCARPESSLTHPHHVLQ 833
 QY 354 QYMEDENTRAYDSSS 368
 Db 834 PHLPKVDYTAQTNS 848

RESULT 4
 PCT-US95-13041-15
 ; Sequence 15, Application PC/TUS9513041
 ; GENERAL INFORMATION:
 ; APPLICANT: WHITE, Morris F.
 ; APPLICANT: SUN, Xiao Jian
 ; APPLICANT: PIERCE, Jacalyn H.
 ; TITLE OF INVENTION: THE IRS FAMILY OF GENES
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13041
 ; FILING DATE: Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/317,310
 ; FILING DATE: 03-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Louis Myers
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: JDP-022PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; PCT-US95-13041-15

Query Match 5.1%; Score 105; DB 5; Length 1234;
 Best Local Similarity 21.0%; Pred. No. 0.36;
 Matches 104; Conservative 57; Mismatches 176; Indels 158; Gaps 25;

QY 1 MEMSGNSGPGHGPQAGSGSTSSSPSGGLMFGQKIYFDDG-----44
 Db 385 VSLSSSTSGHG-STSDCLFRRSSASVSGSPDGGFISDEYSSPCDPSSFRSTVPD 443
 QY 45 -----GSGSS-----SSGGRSNRRVAGSGSGGQIPR 73
 Db 444 SLGHTTPARGEELSNYICMGKASSTLAAPNGHYILSRGGNGHRYIGANLGTSPALPG 503
 QY 74 CQVCGGMDLTMAGYIRHRCVY-----HSTP-KTVVAGIERFCQCCSRF-----121
 Db 504 DEAGAA-DLNR--FRKRTSAGTSPTISHQKTPSOSSVASIEYTEMPLAAYPPGGG 560

QY 122 -----HQLPEFLEKRSRRRLAGHNRERRRPOPASLVSRYGR1APS 166
 Db 561 GGRLPGRHSAPVPTHSEYEEGLEMHLERR-GGHH-----RPPTSNLHT-DDGTPMSP 613
 QY 167 LYENGDAGNNGSFLGNOETMPSSRTLDTRWMRPVSPSQWQNP-----NN 213
 Db 614 ---GVAPVPSNRKQNDY-MPMS-----PKSYAPQOIINPIRRHQRVDPNGYM 660
 QY 214 VFSQGS---VGGRTSFSPPEIMDTKLSY-----KGIDNSNC-ALSLSNPHQ-----258
 Db 661 MSPGSCSPDIGGSSSSSSISAAPSG-SSYCKPWTNGVGHHTHALPHAKPVESGGCK 719
 QY 259 --PHDNNNNNNNNNNNTWRASSGFGPMTVTWAQPPAPSOHQYLNPPVFKDNDNM 316
 Db 720 LLPCTGYMNMSPVGDSTSSPSECYGP-----EDQHKPVLSTYSLPSRFHGTORG 773
 QY 317 SPV-----LNLG-----RY--TEPDNCOISSGTAMG-----EFELSDHHQSR 353
 Db 774 EPEGARHOLRLSSSGRLRYTATAEDSSSTSDSLGGGCGCARPESSLTHPHHVLQ 833
 QY 354 QYMEDENTRAYDSSS 368
 Db 834 PHLPKVDYTAQTNS 848

RESULT 5
 US-08-446-855A-2
 ; Sequence 2, Application US/08446855A
 ; Patent No. 5849573
 ; GENERAL INFORMATION:
 ; APPLICANT: Stewart, Thomas S
 ; APPLICANT: Flores, Maria V
 ; APPLICANT: O'Sullivan, William J
 ; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
 ; TITLE OF INVENTION: phosphate synthetase II
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon & Vanderhye PC
 ; STREET: 1100 No. 5849573th Glebe Road, 8th floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,855A
 ; FILING DATE: 06-Jul-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mitchard, Leonard C
 ; REGISTRATION NUMBER: 29,009
 ; REFERENCE/DOCKET NUMBER: 47-80
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2391 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-855A-2

Query Match 5.1%; Score 105; DB 2; Length 2391;
 Best Local Similarity 26.2%; Pred. No. 0.93;
 Matches 34; Conservative 18; Mismatches 40; Indels 38; Gaps 4;

[illegible]

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RESULT 8
US-08-861-464-6
Sequence 6, Application US/08861464
Patent No. 5874210
GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senescence
TITLE OF INVENTION: In Yeast
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
STREET: Two Militia Drive
City: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MTT-6408A22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-861-464-6
Query Match 5.0%; Score 102; DB 2; Length 888;
Best Local Similarity 26.2%; Pred. No. 0.44;

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REGISTRATION NUMBER: 30,727
 REFERENCE/DOCKET NUMBER: 19603/1741
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1304
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 424 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-120-817-2

Query Match 4.9%; Score 100; DB 4; Length 424;
 Best Local Similarity 20.1%; Pred. No. 0.24;

Matches 83; Conservative 49; Mismatches 128; Indels 152; Gaps 20;

QY 6 NSGPGHGPQAEISGSSSTSSSPSGIMFGQKIYFEDGGG-----SGSSSSGGGRNRRV 60
 DB 117 NNG-GIATPSADSGGGGTPATGAGG---GDTPSATGGGGGTPATGAGGSGGGGTPTA 172
 QY 61 RGGG-----GSGGQIPRCQVEGCGMDLTNAKYRHRVCGVHSTPKYTV----- 107
 DB 173 TGGGSGGTPTATGSGGEGVTPQITPOLANPNRTSGTGSV--DTAGSTEQAGKINVVKOT 230
 QY 108 --AGIEORFCQCCSRF-----HQLPEFLEKRSRRRLAGHNERRRKPPQAS 152
 DB 231 IKVAGAEVFPFHGATFTPADSMGNGDGENQKMFELAEQATLKNV----- 276
 QY 153 LSVLASRYGRHIAFLYENGAGMNGSFLAQOEIGWPSRTLDTRVMRPPVSSPWOINPM 212
 DB 277 -----NLGNEVDGIHVAKNAQEV-----TID-----NVHAQ 304
 QY 213 NVPS-----QSGVGGRITSSSPRIMDTKLESTYKIGDSKCALSLSPHPHDNNNNN 267
 DB 305 NVEEDLITVAGEGAAYTN-----LNIKSSAKGADDK--VQOLNANTLKIKNFK-- 353
 QY 268. NNNNNNNTRASSGFGPMVTMAQPPAPSPQHOLNPNWFKQNDNDMSPV-LNLGRY- 325
 DB 354 -----ADDEGTWRT-----NGKQFDDMSIELNGIEANHGKFA 387
 QY 326 ---TEPDNCOISSGTAMGEFELSDHHQSRROYMEDENTRAYD---SSSHT 371
 DB 388 LVKSDSDDLKLT---ATGNIAMTDVKA-----AYDKTQASTQHT 422

RESULT 15
 US-08-914-999-8
 ; Sequence 8, Application US/08914999
 ; Patent No. 6346406

GENERAL INFORMATION:

APPLICANT: Kyazanov, Alexey G.
 APPLICANT: Hailt, William N.
 TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
 TITLE OF INVENTION: AND METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/914,999

FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 601-1-078
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 732 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Dictyostelium discoideum
 US-08-914-999-8

Query Match 4.9%; Score 100; DB 4; Length 732;
 Best Local Similarity 21.5%; Pred. No. 0.52;

Matches 53; Conservative 28; Mismatches 57; Indels 108; Gaps 11;

QY 168 YENGDAWGNGSFLAQOEIGWPSRTLDTRVMRPPVSSPWOINPMNVFSGSVGGRTSF 227
 DB 242 YNN-----NSGFVSNDRERTPOSFSHT-----YHSHNQLIIDI--QG-VGDHYT-- 285
 QY 228 SPSFIMDTKLESTYKIG-----DSNCAL 250
 DB 286 -----DPQIHVYDGVFGFIGNLGQGFPEKFLDTHKCNALICQYLANIQSINPKSEKSDCGT 339
 QY 251 -----SLSNPHQHNDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 306
 DB 340 VPRPDILPDTSERDNN 375
 QY 307 WFKDNDNMSPYLANIGRYTEPDNCOISSGTAMGEFELSDHHQSRROYMEDENTRAYDS 366
 DB 376 ---NNNNNNSSISKSL-----VEISSGSK---ERRDRSPSPQLRVSN-----DG 414
 QY 367 SSSHTN 372
 DB 415 NTLNTN 420

Search completed: April 10, 2003, 13:54:59
 Job time: 19 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 10, 2003, 13:53:09 ; Search time 20 Seconds
(without alignments)
1146.301 Million cell updates/sec

Title: US-09-839-185-2

Perfect score: 2040
Sequence: 1 MEMGNSGPGHGPQAESEGG.....MEDENTRAYDSSTHTNWSL 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB pep:*
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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2040	100.0	375	10 US-09-839-185-2	Sequence 2, Appl1
2	330	16.2	181	10 US-09-839-185-4	Sequence 4, Appl1
3	321.5	15.8	138	9 US-09-819-142-20	Sequence 20, Appl1
4	306	15.0	848	10 US-09-839-185-8	Sequence 8, Appl1
5	303.5	14.9	174	9 US-09-819-142-8	Sequence 8, Appl1
6	292.5	14.3	131	10 US-09-839-185-6	Sequence 6, Appl1
7	121	5.9	2150	9 US-10-135-322-17	Sequence 17, Appl1
8	120.5	5.9	605	9 US-09-741-233A-2	Sequence 2, Appl1
9	118	5.8	961	10 US-09-801-368-132	Sequence 132, Appl1
10	115	5.6	1569	9 US-10-108-605-303	Sequence 303, Appl1
11	112	5.5	758	10 US-09-801-368-224	Sequence 224, Appl1
12	111.5	5.5	666	10 US-09-801-368-36	Sequence 36, Appl1
13	109	5.3	824	10 US-09-801-368-312	Sequence 312, Appl1
14	107	5.2	411	10 US-09-749-728B-1	Sequence 1, Appl1
15	106	5.2	860	9 US-09-781-693A-2	Sequence 2, Appl1
16	103	5.0	283	10 US-09-864-761-36720	Sequence 36720, A
17	103	5.0	732	9 US-09-832-292-12	Sequence 12, Appl1
18	102	5.0	888	10 US-09-826-752-6	Sequence 6, Appl1
19	101.5	5.0	575	9 US-10-108-605-55	Sequence 55, Appl1

20	100.5	4.9	676	10 US-09-801-368-302	Sequence 302, Appl1
21	100.5	4.9	3092	10 US-09-801-368-172	Sequence 172, Appl1
22	100	4.9	424	10 US-09-835-684-9	Sequence 9, Appl1
23	100	4.9	424	10 US-09-880-371-9	Sequence 9, Appl1
24	100	4.9	424	10 US-09-879-248-14	Sequence 14, Appl1
25	100	4.9	732	10 US-09-994-485-8	Sequence 8, Appl1
26	100	4.9	1207	9 US-10-108-605-71	Sequence 71, Appl1
27	99.5	4.9	861	9 US-09-864-761-109	Sequence 109, Appl1
28	98.5	4.8	357	10 US-09-736-457-1812	Sequence 35807, A
29	98.5	4.8	474	9 US-09-849-626-1812	Sequence 1812, Appl1
30	98.5	4.8	474	9 US-09-849-626-1812	Sequence 1812, Appl1
31	98.5	4.8	474	9 US-09-849-626-1812	Sequence 1812, Appl1
32	98.5	4.8	474	9 US-09-849-626-1812	Sequence 1812, Appl1
33	98.5	4.8	1331	9 US-10-087-464-50	Sequence 50, Appl1
34	98	4.8	623	9 US-10-108-605-125	Sequence 125, Appl1
35	98	4.8	623	9 US-10-108-605-125	Sequence 125, Appl1
36	97.5	4.8	252	9 US-09-880-748-1415	Sequence 1415, Appl1
37	97.5	4.8	440	9 US-09-932-367A-19	Sequence 19, Appl1
38	97.5	4.8	633	9 US-10-086-464-11	Sequence 11, Appl1
39	97	4.8	127	10 US-09-916-940-43	Sequence 43, Appl1
40	97	4.8	251	9 US-09-880-748-1084	Sequence 1084, Appl1
41	97	4.8	386	9 US-10-050-704-100	Sequence 100, Appl1
42	96.5	4.7	570	9 US-09-847-102A-43	Sequence 43, Appl1
43	96	4.7	724	9 US-10-108-603-307	Sequence 307, Appl1
44	96	4.7	645	10 US-09-919-172-41	Sequence 41, Appl1
45	96	4.7	655	10 US-09-205-658-57	Sequence 57, Appl1

ALIGNMENTS

RESULT 1
US-09-839-185-2
Sequence 2, Appl1 Application US/09839185

Patent No. US20020069433A1
GENERAL INFORMATION:

APPLICANT: Schmidt, Edward Daniel Leendert
De Vries, Sape Cornelis

Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SRK

Interacting Proteins
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESS: Syngenta Patent Dept.

STREET: 3054 Cornwallis Road
CITY: RTP

STATE: NC
COUNTRY: USA

ZIP: 27709
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,185

FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: 3A35
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-839-185-2

Query Match 100.0%; Score 2040; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-163;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEMGNSGPGHGPQAGSGSSSTESSFSGGLMFGCKIYFEDGGGSGSSSGGRSNRRV 60
DB 1 MEMGNSGPGHGPQAGSGSSSTESSFSGGLMFGCKIYFEDGGGSGSSSGGRSNRRV 60
QY 61 RGGSGGSGQIPRCQVEGGMGLTNAGYVSRHRYCGVSKTPKTVAGIEORFCQCCSR 120
DB 61 RGGSGGSGQIPRCQVEGGMGLTNAGYVSRHRYCGVSKTPKTVAGIEORFCQCCSR 120
QY 121 FHLPEFLEKSCRRRLAGHNERRRKPPASLVSASHYGRVIAFSLYENGDAAGNGSFL 180
DB 121 FHLPEFLEKSCRRRLAGHNERRRKPPASLVSASHYGRVIAFSLYENGDAAGNGSFL 180
QY 181 GNOETGMPSSRTLDTRVMRRPVSSPMQINPMNVFSGSVGGRTSFSSEPEIMDTKLSY 240
DB 181 GNOETGMPSSRTLDTRVMRRPVSSPMQINPMNVFSGSVGGRTSFSSEPEIMDTKLSY 240
QY 241 KGIGSNCLSLTNSPHOPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
DB 241 KGIGSNCLSLTNSPHOPHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
QY 301 QYLNPPWFKNDNDMSPVNLGRYTEPNCQISSGTAMGEFELSDHHQSRROYMEDEN 360
DB 301 QYLNPPWFKNDNDMSPVNLGRYTEPNCQISSGTAMGEFELSDHHQSRROYMEDEN 360
QY 361 TRAYSSSHHTWML 375
DB 361 TRAYSSSHHTWML 375

RESULT 2
US-09-839-185-4
Sequence 4, Application US/09839185
Patent No. US20020069433A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
CITY: RTP
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: 3B39
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-839-185-4

Query Match 16.2%; Score 330; DB 10; Length 181;
Best Local Similarity 43.4%; Pred. No. 2.1e-20; Indels 34; Gaps 7;
Matches 75; Conservative 22; Mismatches 42; Indels 34; Gaps 7;
QY 45 GSGSSSSGGRSNR-----RVGGSGGSGQIPR--COVEGGMGLTNAGYVSRHRYC 96
DB 29 GMDGEEDGDEDRKKMYERVRG---PSTDVPSRLCQVDRCTVNLTAQYRRHRYC 85
QY 97 GVHSTPRVTYAGIEORFCQCCSRFHQLEPFDLEKSCRRRLAGHNERRRKPPASISVL 156
DB 86 EVHAKASATYAGVGRQFCQCCSRFHELPEFDEAKSCRRRLAGHNERRRK-----IS 138
QY 157 ASRYGRVAPSLYENGDAAGNGSFLGNOEIGWPSRTLDTRVMRR-PVSSPMQ 208
DB 139 GDSFGE-----GSGRRGFSGLQITQE-----NNRVDKLPMTNSSFK 176

RESULT 3
US-09-819-142-20
Sequence 20, Application US/09819142
Publication No. US20030041356A1
GENERAL INFORMATION:
APPLICANT: Reuber, Lynne
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline
APPLICANT: Adam, Luc
TITLE OF INVENTION: Methods for Modifying Flowering Phenotypes
FILE REFERENCE: MBI-0033
CURRENT APPLICATION NUMBER: US/09/819,142
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 138
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-819-142-20

Query Match 15.8%; Score 321.5; DB 9; Length 138;
Best Local Similarity 57.7%; Pred. No. 7.5e-20;
Matches 64; Conservative 11; Mismatches 25; Indels 11; Gaps 3;
QY 45 GSGSSSSGGRSNR-----RVGGSGGSGQIPR--COVEGGMGLTNAGYVSRHRYC 96
DB 29 GMDGEEDGDEDRKKMYERVRG---PSTDVPSRLCQVDRCTVNLTAQYRRHRYC 85
QY 97 GVHSTPRVTYAGIEORFCQCCSRFHQLEPFDLEKSCRRRLAGHNERRRK 147
DB 86 EVHAKASATYAGVGRQFCQCCSRFHELPEFDEAKSCRRRLAGHNERRRK 136

RESULT 4
US-09-839-185-8
Sequence 8, Application US/09839185
Patent No. US20020069433A1

```

GENERAL INFORMATION:
APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
CITY: RTP
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: 3A52
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-839-185-8
Query Match 15.0%; Score 306; DB 10; Length 848;
Best Local Similarity 27.9%; Pred. No. 1,6e-17;
Matches 100; Conservative 44; Mismatches 111; Indels 104; Gaps 13;

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RESULT 5
US-09-819-142-8
Sequence 8, Application US/09819142
Publication No. US20030041356A1
GENERAL INFORMATION:
APPLICANT: Reuber, Lynne
APPLICANT: Ratcliffe, Oliver
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline
APPLICANT: Adam, Luc
TITLE OF INVENTION: Methods for Modifying Flowering Phenotypes
FILE REFERENCE: MBI-0033
CURRENT APPLICATION NUMBER: US/09/819,142
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 174
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-819-142-8
Query Match 14.9%; Score 303.5; DB 9; Length 174;
Best Local Similarity 51.2%; Pred. No. 3.3e-18;
Matches 66; Conservative 13; Mismatches 35; Indels 15; Gaps 4;

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QY 59 RVRG--CGSGGSGQIPRCQVEGCGMDLTNAKGYSRHRYCGVHSTKPKYVAGIEQRFQ 116
DB 37 RVRSRSISIRGSLRCQVDRCTADMKKAKLYHRRKVCVHAKSSVFLSGINORFQ 96
QY 117 QCSRFDLPEDLEKSCRRRLAGHNERRRKPPASLSVLAARYGRIAPSLYENGDAKGN 176
DB 97 QCSRFDLPEDLEKSCRRRLAGHNERRRK-----SSGSEITYG-----GSGRGIN 144
QY 177 GS-FLNGQE 184
DB 145 GQVVMQNGE 153

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RESULT 6
US-09-839-185-6
Sequence 6, Application US/09839185
Patent No. US20020069433A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
CITY: RTP
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 919-541-8587
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: 4B19
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-839-185-6

Query Match          14.3%; Score 292.5; DB 10; Length 131;
Best Local Similarity 58.9%; Pred. No. 1.9e-17;
Matches 53; Conservative 12; Mismatches 27; Indels 3; Gaps 1;

Cy 58 RRVGGGGGSGGQIPRCVGGGMDLTNAKGYSRHVCYHSTPKYTVAGIEORFCQ 117
Db 41 KKQKKAATSSGV---CQVESCADMSKAKQYHKKHVCQFHAKAPHRISGLHORFCQ 97
Cy 118 CSRFHQLPEFDLEKRSRRRLAGHNERRRK 147
Db 98 CSRFHQLSEFDKRSRRRLAGHNERRRK 127

RESULT 7
US-10-135-322-17
; Sequence 17, Application US/10135322
; Patent No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AMM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 2150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-17

Query Match          5.9%; Score 121; DB 9; Length 2150;
Best Local Similarity 26.8%; Pred. No. 0.18;
Matches 37; Conservative 21; Mismatches 64; Indels 16; Gaps 3;

Cy 149 QPAGISVLAARYGRIAPSLYENG---DAGNNGSFLGNOEIMPSSRLDTVMRRPVSS 204
Db 550 QTISEIILGNK-----PYYNNGNNNNNNNNNNSTTNNITNNNNNNNNNNINNVST 604
Cy 205 P-----SWQINPMNVFSGSVGGRTSFSPEIMDTLSEYKIGIGNSCALSLISNPH 257
Db 605 PRKRTKYGHSKTNLSQDEFETSSMNGGDDSIISGAGSGSLRRRNKDDNDENDGNSNNVTNS 664

Cy 258 QPHDNNNNNNNNNNNNNNNN 275
Db 665 NSNNNNNNNNNNNNNNNN 682

RESULT 8
```

```

US-09-741-233A-2
; Sequence 2, Application US/09741233A
; Patent No. US20020157142A1
; GENERAL INFORMATION:
; APPLICANT: Glover, Lynn W.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Zhou, Qing
; APPLICANT: Levin, Joshua Z.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-31127A
; CURRENT APPLICATION NUMBER: US/09/741,233A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-741-233A-2

Query Match          5.9%; Score 120.5; DB 9; Length 605;
Best Local Similarity 21.2%; Pred. No. 0.039;
Matches 89; Conservative 51; Mismatches 163; Indels 117; Gaps 18;

Cy 11 HPGQAESGSGSTSSSFSFSGL-----MFGQKIYFEDGGGSGSSSGGRSNRR 59
Db 226 HFPYGQNTNNNNNNNTSSWILGLSHWGPQNLHQSGDVLRLGSGGGGGAAS---RS- 280
Cy 60 VRGGGSGGSGQIPRCQVGGGMDL--TNAGYSRHVCYHSTPKYTVAGIEORFCQ 117
Db 281 -----SDLIANASGYFWQEQNPSPH-----DQDHHH 308
Cy 118 CSRFHQLPEFDLEKRSRRRLAGHNERRRKQPASLSVLAARYG--RIAPSLYENGDA 175
Db 309 HHHHHQ-----QGFLAGNNNIKQSPMSFQQLMGPFSHNNHNSAPENV-----F 351
Cy 176 NGSL-GENEITGMPSSRTLDTRVMRRPVSSPSWQINPMNVFSGSVGGC----- 224
Db 352 NLSFLSGNN--GVTSATSNPMAAAVAASVSGNLMIS--NHVDGENAVGGGEGSTGLPENN 408
Cy 225 -----TSFSPSEIMDTLSEYKIGIGNSCALSLISNPHQ--PHDNNNNNNNNNN 274
Db 409 LMSADRISSGSVPSLFSSSWQSPNSAPNHS--ATALLQKAAQMGSTSSNNNGSVTNNN 467
Cy 275 NTWBAASGFGPMVTYMAQPPAPSQHOYLNPWFVKDNDMSFV-----LNLGRYTEPD 329
Db 468 NASLIRFGSGIYGENESNLQDLNFSNPGATGNNGVD--SPFGSYGVNKGISADKQ 526
Cy 330 NCQ-----ISSGTAMGEFELSDHHHQRQRYMEDNTR-----AYDSSAHTN 372
Db 527 SMTRDFLGQIVKSMGSGGFGQOQOQOQOQOQOQOQOQHGNRERVGSSSDADRSSNNVN 586

RESULT 9
US-09-801-368-132
; Sequence 132, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
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[illegible]

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: Sequence 1, Application US/0
: Patent No. US20020142457A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Umezawa, Akihito
: APPLICANT: Hata, Jun-ichi
: APPLICANT: Fukuda, Keiichi
: APPLICANT: Ogawa, Satoshi

```


Query March 5.2% Score 106; DB 9; Length 860;
 Best Local Similarity 19.8%; Pred. No. 1;
 Matches 83; Conservative 57; Mismatches 182; Indels 98; Gaps 15

5 SMSGPHGP-GQAESGSGSTESSFFSGCLMFQGXIFEDGCGGSGSSSGGRENRRVGG 63
 ||:| | : : : : : ||: | : | | |

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Search completed: April 10, 2003, 13:55:25
Job time : 25 secs
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GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2003, 13:51:09 ; Search time 35 Seconds
(without alignments)
2207,648 Million cell updates/sec

Title: US-09-839-185-2

Perfect score: 2040

Sequence: 1 MEMGNSGPGHGPQAEISGG.....MEDENTRAYDSSSHHTWISL 375

Scoring table: BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhcc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2033	99.7	375	10	048527 arabidopsi
2	2009.5	98.5	374	10	0944J2 arabidopsi
3	1956	95.9	373	10	09SMX7 arabidopsi
4	863.5	42.3	354	10	09M206 arabidopsi
5	615	30.1	323	10	09SNV3 arabidopsi
6	556	27.3	257	10	09SNV4 arabidopsi
7	417	20.4	329	10	09SM15 arabidopsi
8	400	19.6	425	10	09SMY0 arabidopsi
9	396	19.4	359	10	09LUF4 arabidopsi
10	392	19.2	419	10	09S840 arabidopsi
11	374.5	18.4	394	10	0947M8 arabidopsi
12	374.5	18.4	405	10	09S7A2 arabidopsi
13	365.5	17.9	378	10	09LOA4 arabidopsi
14	356	17.5	392	10	09FZJ9 arabidopsi
15	356	17.5	396	10	09ZWS3 arabidopsi
16	356	17.5	396	10	08S910 arabidopsi

17	354.5	17.4	389	10	09FZK0 arabidopsi
18	354.5	17.4	393	10	09ZW54 arabidopsi
19	351	17.2	367	10	09SM14 zea mays (m
20	334	16.4	435	10	09SM17 arabidopsi
21	333	16.3	333	10	09S849 arabidopsi
22	330	16.2	181	10	09S758 arabidopsi
23	328.5	16.1	1020	10	09C9K0 arabidopsi
24	327.5	16.1	424	10	09SM16 zea mays (m
25	326.5	16.0	440	10	09SM19 zea mays (m
26	321.5	15.8	138	10	09SMW8 arabidopsi
27	321	15.7	927	10	09S7P5 arabidopsi
28	318.5	15.6	1035	10	09S7N9 arabidopsi
29	313	15.3	305	10	09SMV5 arabidopsi
30	311.5	15.3	445	10	09SM18 zea mays (m
31	310	15.2	881	10	082651 arabidopsi
32	309	15.1	881	10	09SMX9 arabidopsi
33	303.5	14.9	167	10	09SMX8 arabidopsi
34	303.5	14.9	174	10	09S7A9 arabidopsi
35	297	14.6	240	10	080718 arabidopsi
36	292.5	14.3	129	10	09LFB4 arabidopsi
37	292.5	14.3	131	10	P93015 arabidopsi
38	283	13.9	862	10	09LGV7 arabidopsi
39	272	13.4	131	10	09SM13 zea mays (m
40	255.5	12.5	377	10	09SMY1 arabidopsi
41	254.5	12.5	775	10	08VZV0 arabidopsi
42	254.5	12.5	789	10	08S9G8 arabidopsi
43	254.5	12.5	801	10	09S7Z3 arabidopsi
44	169	8.3	662	5	08TIP5 dicotyrel
45	160.5	7.9	816	5	024538 drosophila

ALIGNMENTS

RESULT 1
ID 048527 PRELIMINARY; PRT; 375 AA.
AC 048527;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative squamosa-promoter binding protein.
GN T24P15.11 OR SPL9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Kaul S., Mason T.M., Keiravage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=97446501; PubMed=9301089;
RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
RT "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
RL novel gene involved in the floral transition.";
RL Plant J. 12:367-377 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=99453765; PubMed=10524240;
RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
RA Huijser P.;
RT "Molecular characterization of the Arabidopsis SBP-box genes.";
RL Gene 237:91-104 (1999).
DR EMBL; AC002561; AAB88645.1; -;
DR EMBL; AJ011640; CAB56592.1; -;

DR EMBL: AJ011638; CAB56590.1; -;
 DR InterPro: IPR004333; SBF_plant_prot.
 DR Pfam: PF03110; SBF; 1.
 SQ SEQUENCE 375 AA; 40846 MW; DLB93F98BD0ECD28 CRC64;

Query Match 99.7%; Score 2033; DB 10; Length 375;
 Best Local Similarity 99.7%; Pred. No. 3.5e-153;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60
 DB 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60
 QY 61 RGGSGGSGQIPRCOVGCGMDLTNAKGYSRHRCVGHSTPKYTVAGIEQRCCQCSR 120
 DB 61 RGGSGGSGQIPRCOVGCGMDLTNAKGYSRHRCVGHSTPKYTVAGIEQRCCQCSR 120
 QY 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 DB 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 QY 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 DB 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 QY 181 GNOETGWPSSRTLDTRVKRRPVSSPQWQINPMNVFSQSGVGGGTSSPSPIMDTKLESY 240
 DB 181 GNOETGWPSSRTLDTRVKRRPVSSPQWQINPMNVFSQSGVGGGTSSPSPIMDTKLESY 240
 QY 241 KGIGDGNCLSLNSPHQPHDNNNNNNNNNTWRASGFGPMVTYMAQPPAPSOH 300
 DB 241 KGIGDGNCLSLNSPHQPHDNNNNNNNNNTWRASGFGPMVTYMAQPPAPSOH 300
 QY 301 QYLNPPWFVKDNDMSFVLNLGRYTEPDNCQISSGTAMGEFELSDHHHSRQYMEDN 360
 DB 301 QYLNPPWFVKDNDMSFVLNLGRYTEPDNCQISSGTAMGEFELSDHHHSRQYMEDN 360
 QY 361 TRAYDSSSHHTNWSL 375
 DB 361 TRAYDSSSHHTNWSL 375

RESULT 2

Q94AJ2 PRELIMINARY; PRT; 374 AA.

AC Q94AJ2
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Putative squamosa-promoter-binding protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX [1]
 RN [1]
 RP SEQUENCE FROM N. A.
 RC YANADA K., LIU S.-X., PHAM P.-K., BANH J., DALE J.M., GIBSON H.A.,
 RA GOLDMITH A.D., JIANG P.-X., LEE J.M., ONODERA C.S., QUACH H.L.,
 RA TANG C., TORIUMI M., YU G.-Y., BOWSER L., CARLINI P., CHEN H.,
 RA CHEN R., HAYASHIZAKI Y., ISHIDA J., JONES T., KARIYA A.,
 RA KARLIN-NEUMANN G., KAWAI J., KIM C., KOSEMA E., LAM B., LIN J.,
 RA MEYER M.C., MIRANDA M., NARUSAKA M., NGUYEN M., PALM C.J.,
 RA SAKURAI T., SATOU M., SEKI M., SHIN P., SOUTHWICK A., TRACY S.E.,
 RA SHINOZAKI K., DAVIS R.W., ECKER J.R., THEOLOGIS A.,
 RT "Full length cDNA of gene T24P15.11/At2g42200 (GI:2673911)."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY046007; AAK76681.1; -;
 DR InterPro: IPR004333; SBF_plant_prot.
 DR Pfam: PF03110; SBF; 1.
 SQ SEQUENCE 374 AA; 40733 MW; EAC1C38200E5386 CRC64;

Query Match 98.5%; Score 2009.5; DB 10; Length 374;
 Best Local Similarity 99.2%; Pred. No. 2.6e-151;
 Matches 372; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60

DB 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60
 QY 61 RGGSGGSGQIPRCOVGCGMDLTNAKGYSRHRCVGHSTPKYTVAGIEQRCCQCSR 120
 DB 61 RGGSGGSGQIPRCOVGCGMDLTNAKGYSRHRCVGHSTPKYTVAGIEQRCCQCSR 120
 QY 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 DB 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 QY 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 DB 121 FHLPEPFLERKSCRRLAGNERRRKQPASLSVLSRYRIAPSLYENGDAWNQSF 180
 QY 181 GNOETGWPSSRTLDTRVKRRPVSSPQWQINPMNVFSQSGVGGGTSSPSPIMDTKLESY 240
 DB 181 GNOETGWPSSRTLDTRVKRRPVSSPQWQINPMNVFSQSGVGGGTSSPSPIMDTKLESY 240
 QY 241 KGIGDGNCLSLNSPHQPHDNNNNNNNNNTWRASGFGPMVTYMAQPPAPSOH 300
 DB 241 KGIGDGNCLSLNSPHQPHDNNNNNNNNNTWRASGFGPMVTYMAQPPAPSOH 300
 QY 301 QYLNPPWFVKDNDMSFVLNLGRYTEPDNCQISSGTAMGEFELSDHHHSRQYMEDN 360
 DB 301 QYLNPPWFVKDNDMSFVLNLGRYTEPDNCQISSGTAMGEFELSDHHHSRQYMEDN 360
 QY 361 TRAYDSSSHHTNWSL 375
 DB 361 TRAYDSSSHHTNWSL 374

RESULT 3

Q9SMX7 PRELIMINARY; PRT; 373 AA.

AC Q9SMX7
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Squamosa promoter binding protein-like 9.
 GN SPL9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX [1]
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=CV, LANDSBERG ERECTA; TISSUE=FLOWER;
 RC MEDLINE=99453765; Pubmed=10524240;
 RA CARDON G.H., HOEHMANN S., KLEIN J., NETTESHEIM K., SAEDLER H.,
 RA HUIJZER P.;
 RT "Molecular characterization of the Arabidopsis SBF-box genes";
 RL Gene 237:91-104(1999)
 DR EMBL: AJ011639; CAB56591.1; -;
 DR InterPro: IPR004333; SBF_plant_prot.
 DR Pfam: PF03110; SBF; 1.
 SQ SEQUENCE 373 AA; 40552 MW; 3B97A844659B2579 CRC64;

Query Match 95.9%; Score 1956; DB 10; Length 373;
 Best Local Similarity 96.1%; Pred. No. 4.4e-147;
 Matches 366; Conservative 0; Mismatches 1; Indels 14; Gaps 2;

QY 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60
 DB 1 MEMGNSGPGHGPQAGSSTSSSFSGGLMFQKTYFEDGGGSGSSGGRSNRV 60
 QY 61 RGGSGGSGQIPRCOVGCGMDLTNAKGYSRHRCVGHSTPKYTVAGIEQRCCQCSR 120

Db 61 RGGSGGSGGQIPRCQVCGCGMDLTNAKGYSSRRHVCVGHSTKPTVAGLEQRFCCQCSR 120

Qy 121 PHQPEPDLKRSGRRLAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFL 180

Db 121 PHQPEPDLKRSGRRLAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFL 180

Qy 181 GNOEIGMPSSRTLDTRVRRPVSPPSQINPMNVFSGSVGGTFSFSPPEIMDTKLESY 240

Db 181 GNOEIGMPSSRTLDTRVRRPVSPPSQINPMNVFSGSVGGTFSFSPPEIMDTKLESY 240

Qy 241 KGIGDSNCALSLSNPQPHD-----NNNNNNNNNNNTWRASSGFGPMVTYMAQPP 294

Db 241 KGIGDSNCALSLSNPQPHDNNNNNNNNNNNNNNNNNNNNNTWRASSGFGPMVTYMAQPP 300

Qy 295 PAPSQHQYLPMPVFKXNDNDMSFVLNIGRTYEPDNCQISSGTAMGEFELSDHHQSRQ 354

Db 301 PAPSQHQYLPMPVFKXNDNDMSFVLNIG-----QISSGTAMGEFELSDHHQSRQ 352

Qy 355 YMEDENTRAYDSSSHHTWML 375

Db 353 YMEDENTRAYDSSSHHTWML 373

RESULT 4

Q9M206 PRELIMINARY; PRT; 354 AA.

AC Q9M206;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Squamosa promoter-binding protein homolog.

GN T10K17.130.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_Taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Benes V., Wurmbach E., Drzonek H., Ansgorge W., Mewes H.W., Lemcke K.,

RA Meyer K.F.X., Queller F., Salanoubat M.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [2];

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL132977; CAB67620.1;

DR InterPro; IPR004333; SBP_plant_prot.

DR Pfam; PF03110; SBP; 1.

SQ SEQUENCE 354 AA; 39672 MW; F84HD9DFC9CB85 CRC64;

Query Match 42.3%; Score 863.5; DB 10; Length 354;

Best Local Similarity 52.7%; Pred. No. 1.5e-60;

Matches 204; Conservative 32; Mismatches 86; Indels 65; Gaps 17;

Qy 14 GQASGSG-SSTSSSFSGGLMGOKIYEPDGGGSGSSSGSRNRVRGGSGGSGQIP 72

Db 8 GQASGSGSSSTSSSLGGLRFGQKIYEDG-----SGSRNRVR-----NTWRASSTTA 57

Qy 73 RCQVCGCGMDLTNAKGYSSRRHVCVGHSTKPTVAGLEQRFCCQCSRPHQPEPDLKRS 132

Db 58 RCQVCGCGMDLTNAKGYSSRRHVCVGHSTKPTVAGLEQRFCCQCSRPHQPEPDLKRS 117

Qy 133 SCRRRLAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFLGNOEIGMPSSRT 192

Db 118 SCRRRLAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFLGNOEIGMPSSRT 175

Qy 193 LQTRVRRPVSPPSQINP-----NMVFGSGSVGGRTSPSS-PEIMDTKLESYKIG 244

Db 176 ----YMQRP-----GPMQINPVEETHPHMVLNHS-----SFTTPEMINNST----- 217

Qy 245 DSNCAILSLSNPQPHDNNNNNNNNNNNNNNNNNNNTWRASSGFGPM-----TVTMAQPP 293

Db 218 DSSCALSLSNPPIH-----QQQLQTPNTWRPSSGFDMSISFDKTYMAQPPPISTH 271

Qy 294 -PAPSQHQYLPMPVFK-----KXNDNDMSFVLNIGRTYEPDNCQISSGTAMGEFELSDHH 348

Db 272 QPPISTHQQYLSQTWIAGNERKSNHMSPV-----SQISEPADQISNGTMSGFELY-LH 327

Qy 349 HQSRROYMEDENTRAYDSSSHHTWML 375

Db 328 QOYLKQYMEDENTRAYDSSSHHTWML 354

RESULT 5

Q9SNV3 PRELIMINARY; PRT; 323 AA.

AC Q9SNV3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Squamosa promoter binding protein-homologue 5 (fragment).

GN SBPH5.

OS Antirrhinum majus (Garden snapdragon).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.

OX NCBI_Taxid=4151;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=FLOWER;

RA MEDLINE=97446501; PubMed=9301089;

RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huiser P.;

RT "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a

RT novel gene involved in the floral transition."

RL Plant J. 12:367-377 (1997).

RN [2];

RP SEQUENCE FROM N.A.

RC TISSUE=FLOWER;

RA MEDLINE=99453765; PubMed=10524240;

RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,

RA Huiser P.;

RT "Molecular characterization of the Arabidopsis SBP-box genes.";

RT Gene 237:91-104 (1999).

DR EMBL; AU011623; CAB56570.1;

DR InterPro; IPR004333; SBP_plant_prot.

DR Pfam; PF03110; SBP; 1.

FT NON TER 1 1

SQ SEQUENCE 323 AA; 35124 MW; D2587CFB96A38BF CRC64;

Query Match 30.1%; Score 615; DB 10; Length 323;

Best Local Similarity 40.0%; Pred. No. 6.5e-41;

Matches 154; Conservative 50; Mismatches 91; Indels 90; Gaps 18;

Qy 18 SGGSTSSSFSGGLMGOKIYEPDGGGSGSSSGSRNRVRGGSGGSGQIPRCQV 77

Db 2 AAGAEERSLN---GLKRGKITYEEARAKKKGSTG-----VRCQVE 41

Qy 78 GCGMDLTNAKGYSSRRHVCVGHSTKPTVAGLEQRFCCQCSRPHQPEPDLKRSGR 137

Db 42 GCEYDLSDARAYIRHRYVCSMHSKSPVYIAGIQRCQCSRPHQPEPDLKRSGR 101

Qy 138 LAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFLG-----QELGWS 189

Db 102 LAGNERRRKQPASLSVLASRYGRAPSLYENGDAAGMSFLG-----QELGWS 157

Qy 190 SRTLDTRVRRPVSPPSQINP-----NPMNVFGSGSVGGRTSPSSPEIMDTKLESYKIG 246

Db 158 --TIPBGLGQPS--PWQDMQNPVEFLRGTT--NRPSFGIGV--SSEECFSGVNS 209

Qy 247 NCALSLSNPQPHDNNNNNNNNNNNNNNNNNNNTWRASSGFGPMVTYMAQPP--PAPSQHQYLN 304

Db 210 STALSLSN--QSWGSRNSNPLGTNG-----GP---TIVQISINCATIGFTC 255

Qy 305 PPWFVKDN--DN---DMSPVNLIGRYT-----EPDNCQISSGTAMGEFELSDHHQ 350

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Db 256 PSWGGNGNPADNTSHDMPNLTGQFSSNSHNTGEBGVQLSHG----- 301
Oy 351 SRQYMEDENTRAYDSSSHHTNWSL 375
Db 302 ---QFQDLDHSHRGYDSSVQDMHMSL 323

RESULT 6
O9SNV4 PRELIMINARY; PRT; 257 AA.
ID O9SNV4
AC O9SNV4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Squamosa promoter binding protein-homologue 4 (Fragment).
GN SBH4.
OS Antirrhinum majus (garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asceridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxId=4151;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RX MEDLINE=97446501; PubMed=9301089;
RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
"Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
RT novel gene involved in the floral transition.";
RL Plant J. 12:367-377(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RX MEDLINE=99453765; PubMed=10524240;
RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
Huijser P.;
"Molecular characterization of the Arabidopsis SBP-box genes.";
RL Gene 237:91-104(1999).
DR EMBL; AJ011622; CAB56569.1;
DR InterPro; IPR004333; SBP_plant_prot.
DR Pfam; PF03110; SBP; 1.
FT NON_TER 1
SQ SEQUENCE 257 AA; 27692 MW; 39869PEBA547635A CRC64;

Query Match 27.3%; Score 556; DB 10; Length 257;
Best Local Similarity 49.4%; Pred. No. 2.3e-36;
Matches 127; Conservative 37; Mismatches 73; Indels 20; Gaps 8;

Oy 25 SSSFGGLMFGQKTYFEDGGGSSSSGGSNRRYRGSGSQGQIPRCQVGGCMT 84
Db 4 SSSSLNGLNFGRKTYFEN-VGSSGLQSS--PSKGRSGGVVQGGQPPRCQVEGCKIDLS 59
Oy 85 NAKGYSHRHVGVSKTPKTVAGIEGRFCQCGSRFHQLPEFDLEKSCRRRLAGHNER 144
Db 60 DAKATYSRHKVGMSKSKVIVAGIEGRFCQCGSRFHQLPEFDLEKSCRRRLAGHNER 119
Oy 145 RRPQPAISLVASRYGRIAPSLYENGDAKMGSPFLGNQEIWPS-----SRTLDTRV 197
Db 120 RRRPFP--VSTISPRYGSLSPTIFDN--YSKPGFVLDPSSSHPNLTGKDSMANTSSERG 175
Oy 198 MKRPVSSPQWQINPMNVPSQSGVGGRTSFSSPEIMDTLSEYKGI-GDSNCALSLSNP 256
Db 176 LGNQLSMQSNSQNPPLPDFLQGSSTSRPSYSGHV--SSVECFGVSSPDSGALSLSN- 232
Oy 257 HPHNNNNNNNNNNNN 273
Db 233 -QPWGSRTRASSLGLNN 248

RESULT 7
O9SM15 PRELIMINARY; PRT; 329 AA.
ID O9SM15
AC O9SM15
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE SBP-domain protein 5 (fragment).
GN SBP5.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_7232; TISSUE=EARLY FEMALE INFLORESCENCE;
RX MEDLINE=97446501; PubMed=9301089;
RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
"Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
RT novel gene involved in the floral transition.";
RL Plant J. 12:367-377(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_7232; TISSUE=EARLY FEMALE INFLORESCENCE;
RX MEDLINE=99453765; PubMed=10524240;
RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
Huijser P.;
"Molecular characterization of the Arabidopsis SBP-box genes.";
RL Gene 237:91-104(1999).
DR EMBL; AJ011618; CAB56631.1;
DR InterPro; IPR004333; SBP_plant_prot.
DR Pfam; PF03110; SBP; 1.
FT NON_TER 1
SQ SEQUENCE 329 AA; 34775 MW; CE44BE2583C8FD83 CRC64;

Query Match 20.4%; Score 417; DB 10; Length 329;
Best Local Similarity 35.9%; Pred. No. 3.2e-25;
Matches 127; Conservative 46; Mismatches 97; Indels 84; Gaps 21;

Oy 73 RCQVGGCMTDTNKK-GYSHRRVGVSKTPKTVAGIEGRFCQCGSRFHQLPEFDLEK 131
Db 9 RCQVGGCMTDTNKK-GYSHRRVGVSKTPKTVAGIEGRFCQCGSRFHQLPEFDLEK 68
Oy 132 RSCRRRLAGHNERRRRPPQPAISLVASRYGRIAPSLYENGDAKMGSPFL-----GN 182
Db 69 KSCRRRLAGHNERRRRPPQPAISLVASRYGRIAPSLYENGDAKMGSPFL-----GN 122
Oy 183 QEIGWSSSRTLDTRVMRRPVSSPSWQ--INPMNVPSQGV-----GGRTSFSSP 230
Db 123 MRGPFVAVRPGSERV---PGGIQWAGLDPRH--HQGAVAGYGAHYGSEGGSSSARPP 176
Oy 221 EIMDTKLE---SYKGI-GDSNCALSLSNPHQPHDNNNNNNNNNNNTWRASSGFGPM 286
Db 177 VFPGEPLPPGGCLAGVPADSSCALSLST--QPWDAAHSHSHA-----APTAGFD- 226
Oy 287 TVTMAQPPAPAS---QHQYLPN-PWVFKDNDNMSPVNLGR---YTEPDC--QISSG 336
Db 227 ---GGSVVASLSMAASVITAPSWTEIDTSWGHEG-----GRSPQLRPDDVPLGEVNSG 277
Oy 337 TA-----MGEFELSDHHQ-----SRQYMEDENTRAYDSSSHHTNWSL 375
Db 278 SSSHHGQSGSELELALQGNRPAPGSAAPAPARNNGSAGT--PDQAGTMDWSL 329

RESULT 8
O9SMY0 PRELIMINARY; PRT; 425 AA.
ID O9SMY0
AC O9SMY0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Squamosa promoter binding protein-like 2.
GN SPL2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, LANDSBERG, ERECTA; TISSUE=FLOWER;
RX MEDLINE=97446501; PubMed=9301089;
RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
RT "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
RT novel gene involved in the floral transition.";
RL Plant J. 12:367-377(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, LANDSBERG, ERECTA; TISSUE=FLOWER;
RX MEDLINE=99453765; PubMed=10524240;
RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
RA Huijser P.;
RT "Molecular characterization of the Arabidopsis SBP-box genes.";
RL Gene 237:91-104(1999).
DR EMBL; AU011625; CAB56577.1; -
DR InterPro; IPR004333; SBP_plant_prot.
DR Pfam; PF03110; SBP.1.
SQ SEQUENCE 425 AA; 47404 MW; 4D2AE7637BAE404A CRC64;

Query Match 19.6%; Score 400; DB 10; Length 425;
Best Local Similarity 31.0%; Pred. No. 9.9e-24;
Matches 120; Conservative 51; Mismatches 108; Indels 108; Gaps 17;

QY 13 PGAGESG---GSTSSSFGS---GLMFGQKIYFED---GGGSGS-----SSSSG 53
DB 97 PGEAKCIDTSPTEILSPGSDPVLGLTKRKYFEDFEVENAKGLPYSLASSVSP 156
QY 54 GRSNRVRGGSGSGQIPRCQVCGMDLTNAKYYSRRHRCVGHKTPKTVAGIEOR 113
DB 157 VKSKSI-----PRLTPHCQVCGMDLSSADYHKKRHCENHKKSPRVVSGVER 211
QY 114 FCGCCSFHQLPEFDLEKSCRRRLAGHERRRRKPPA-----SLSLASRGRAP 166
DB 212 FCGCCSFHCLSEFDEKSCRRRLSDHARRRPNRRTYDGRPOVDVFNRRPALHPR 271
QY 167 LYENGDAAGNAGFLGNELGMPSSRTLDTRWARRPVSQIMPMVFGSGSGV---G 223
DB 272 SEB-----KFL-----WSSKVPVSRVL---MPQALTEISNKLFEHSHFGLDP 314
QY 224 RTSFSSPEIMDK---LESYKIG-DSNCALSLSNPHQPHDNNNNNNNNNNNTWRA 279
DB 315 KTSARAEALPSKEKVTISSHWGAQDLDGALSLSS-----NSTW-V 355
QY 280 SSGFGPMTVTAOPPPAPSOHQYINPMPVKDNDMSPLV-----LGRYTEPNC 331
DB 356 SSSDQPRRFTLDHPR-----SSNLOPIANRGAQLSVSGYQDPDPP 397
QY 332 QISSGTAMGEFELSDHHQSRQYMED 358
DB 398 AVEGPTAL-----HNGAGQENEN 416

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RESULT 9

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ID Q9LUF4 PRELIMINARY; PRT; 359 AA.
AC Q9LUF4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similarity to equimosa promoter binding protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,

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RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RT Submitted (APR-1999) to the EMBL/Genbank/DBD databases.
DR EMBL; AB023037; BAA96980.1; -
DR EMBL; AB025619; BAB09142.1; -
DR InterPro; IPR004333; SBP_plant_prot.
DR Pfam; PF03110; SBP.1.
SQ SEQUENCE 359 AA; 39108 MW; D80B8B9FD03D349F CRC64;

Query Match 19.4%; Score 396; DB 10; Length 359;
Best Local Similarity 34.7%; Pred. No. 1.7e-23;
Matches 115; Conservative 31; Mismatches 77; Indels 108; Gaps 15;

QY 4 GSNSGCHGP---QASGSGSTSSSFGGLMFGQKIYFEDGGSGSSS-----52
DB 14 GFQEPDLSMDSISFGSGSKADFSFDLKLGRNI-----GNSSVFGDTQYI 64
QY 53 -----GGR---SNRRVRGGSGSGQIPRCQVCGMDLTNAKYYSRRHRC 96
DB 65 SLKMKDSALAKREGSRSSSKTRNGVC-TNQMPLCLVDGSDSPSNCRERHKKHYC 123
QY 97 GVHAKTPKTVAGIEORFCQCGSRFHQLPEFDLEKSCRRRLAGHERRRRKPPAPASLV 156
DB 124 DVHAKTPVVTINGHQRFCQCGSRFHALFEFDGKSCRRRLDGHRRRRKPPPEHI--- 180
QY 157 ASRYGRAPLYENGDAAGNAGS---FLGNELGMPSSRTLDTRWARRPVSQIMPMV 210
DB 181 -----GRPA-----NFTFGGSKLLEFGSGSHV-FPTSVL-----NDSWNSLV 220
QY 211 PMNVFGSGSVGGRTSP-----SSPEIMDKLESY-----240
DB 221 SVAVANAGSSYGOSQSVVSSSPAKTGIMFPISSPRSTSIKQPFLOEESSTASL 280
QY 241 -----KGIQDNCALSLSN-----PH--QP 259
DB 281 CERNITCIIHSDCALSLSSSSSVPHLQP 311

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RESULT 10

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ID Q9S840 PRELIMINARY; PRT; 419 AA.
AC Q9S840;
DT 01-MAY-2000 (T-EMBlrel. 13, Created)
DT 01-MAY-2000 (T-EMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Squamosa promoter binding protein-like 2.
GN SPL2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA; TISSUE=INFLORESCENCE;
RX MEDLINE=97446501; PubMed=9301089;
RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
RT "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
RT novel gene involved in the floral transition.";
RL Plant J. 12:367-377(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA; TISSUE=INFLORESCENCE;
RX MEDLINE=99453765; PubMed=10524240;

```

RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
 RA Huijser P.,
 RT "Molecular characterization of the Arabidopsis SBP-box genes.",
 RL Gene 237:91-104(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=9937451; PubMed=10470850;
 RA Kaneo T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT pl and TAC clones.",
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AJ011626; CAB56578.1; -
 DR EMBL; AJ011624; CAB56576.1; -
 DR EMBL; AB017070; BAB10590.1; -
 DR InterPro; IPR004333; SBP_plant_prot.
 DR Pfam; PF03110; SBP; 1.
 SQ SEQUENCE 419 AA; 46660 MW; 092C3A1DF034EBFF CRC64;

Query Match 19.2%; Score 392; DB 10; Length 419;
 Best Local Similarity 31.5%; Pred. No. 4.2e-23;
 Matches 116; Conservative 49; Mismatches 111; Indels 92; Gaps 16;

QY 13 PQAESG---GSSTSSSSSG---GLMFGQKTYFD-----GGGSG-----SSSG 53
 Db 94 PQEPAKIDTSPSLSLFSGSGDPVLGLKLGKRTYFEDFWEVENAKGLGLPVLASSVSP 153
 QY 54 GRSNRVVGSGSGGQIPRCVGECCMDLTNAKGYSRHRRCVHSTKPTVAGIEOR 113
 Db 154 VKSSSI-----PQLQTPHCQVECNLDLSSAKDYHRKRIICENHSKPKVVGVERR 208
 QY 114 FCQCCSRFHOLPEFLERKSCRRRLAGHNERRKPOPA-----SLSLVLSRYGRIAPS 166
 Db 209 FCQCCSRFHCLSEFPBKRSRRRLSDHNAKRRKPNPGRTYNGKQVDFVNRFLIHR 268
 QY 167 LYENDAGMNGSFLNQGRTGWPSSRTLDTRY--MRPVSS--PSWQINPMWVFSQSGVGG 223
 Db 269 -----SEKRTWPSSKHVPSRVLMPOAKTEISDTENRGLDLPKTKAR 314
 QY 224 RTSFSSPEIMDTKLESYKIG--DSNCALSLSLNPHQPHDNNNNNNNNNNNTTRASSG 282
 Db 315 AELFEKERV---TISHHMGASQDLGALSLS-----NSTTV-VSSS 352
 QY 283 FGPMVTMAQPPPA---PSOHQYLNPPWFKNDNDMSVNLGRYTEPDNCQISSGTAM 339
 Db 353 DQPRFTLDHSSSLVQPVNHR-----SAAQLNSVSGVMQDPDPAVAGPTRL 399
 QY 340 -----GEF 342
 Db 400 HRNGVGQF 407

RESULT 11

Q94JW8 PRELIMINARY; PRT; 394 AA.

AC Q94JW8;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Similar to squamosa-promoter binding protein 1 isoform
 DE gi11707009.
 GN F4N2.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RN NCB1_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Chen H., Cheuk R.,

RA Chung M.K., Kim C., Lin J., Liu S.X., Pham P.K., Sakano H., Shinn P.,
 RA Yamada K., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370612; AAK4391.1; -
 DR InterPro; IPR004333; SBP_plant_prot.
 DR Pfam; PF03110; SBP; 1.
 SQ SEQUENCE 394 AA; 44636 MW; 9ABFC7F8B7DED9 CRC64;

Query Match 18.4%; Score 374.5; DB 10; Length 394;
 Best Local Similarity 32.4%; Pred. No. 9.5e-22;
 Matches 122; Conservative 38; Mismatches 139; Indels 77; Gaps 14;

QY 15 QAESGSSSTSSSGGLMFGQKTYFE-----DGGGSGSSSGGRNRRVGGSGSQSG 69
 Db 51 EEBDEINISSSKFSSQEL--NRIDFKLSFLDGNDDDTSSRGFALPSKSRASICS 108
 QY 70 QIPRCVGECCMDLTNAKGYSRHRRCVHSTKPTVAGIEGFCQCCSRFHOLPEFL 129
 Db 109 QNPLQVYGGCKSLSSSKDYHKKRIVCEAHSTISVIVNGLEQRFCCQCCSRFHLSERDD 168
 QY 130 EKRCRRRLAGHNERRRKPPASLSVLSRYGRIAPSLYENDAGMNGSFLNQGRTGWP 189
 Db 169 GKRCRRRLAGHNERRRK--PAFYFLPKRH-----KLTRTSQDVGNKFLNSSLVLP 221
 QY 190 S-----RTLDTRYMR--RPVS--PSWQINPMWVFSQSGVGGRTSPSSPEIMDTKL 237
 Db 222 SFPGLYRVIVDEDHRTSRLVSFKDEPTCSMFPTN--EONS---SRTYESKPAIYSTEV 276
 QY 238 ESYKIGD-----SNCALSLSLNPHQPHDNNNNNNNNNNNTTRASSGSGFG 284
 Db 277 SINDLHETASRSTRALSLSAOSQHLSEFPNTTSITOPNOLNHSST----- 328
 QY 285 PMVTMAQPPPAPOHQLNPPWFKNDNDMSVNLGRYTEPDNCQISSGTAMGEFEL 344
 Db 329 -----DYHQEGQLWIDPKTNSAG-----SSCKGKGTSTVDLQL 365
 QY 345 SDH--HHOSRQVWED 358
 Db 366 SSHLQRIEQQRNYTGD 381

RESULT 12

Q9S7A2 PRELIMINARY; PRT; 405 AA.

AC Q9S7A2;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Squamosa promoter binding protein-like 6.
 GN SPL6 OR F23010.24.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RN NCB1_TaxID=3702;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=97446501; PubMed=9301089;
 RA Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser P.;
 RT "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a
 RT novel gene involved in the floral transition.",
 RL Plant J. 12:367-377(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=99453765; PubMed=10524240;
 RA Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H.,
 RA Huijser P.;
 RT "Molecular characterization of the Arabidopsis SBP-box genes.",
 RL Gene 237:91-104(1999).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=Cv. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Roming C.M., Koo H., Fujii C.Y., Uteback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome 1 BAC F23010 genomic sequence."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ011644; CAB56596.1;
 DR EMBL; AJ011643; CAB56595.1;
 DR EMBL; AC018364; AAC52487.1;
 DR InterPro; IPR004333; SBP_plant_prot.
 DR Pfam; PF03110; SBP; 1
 SQ SEQUENCE 405 AA; 45952 MW; B7DD1356C6DEE259 CRC64;

Query Match 18.4%; Score 374.5; DB 10; Length 405;
 Best Local Similarity 32.4%; Pred. No. 9.8e-22;
 Matches 122; Conservative 38; Mismatches 139; Indels 77; Gaps 14;

QY 15 QAESGSGSTSSSSFGGLMGOKIYFE-----DGGGSGSSSGGSRNRRVGGGSGSG 69
 Db EEBEENISSSKFSSQEL--NRIDFKLSFLDIGNDDDDSSRGFALPSKSRASNLCS 119
 QY 70 QIPRCVGGGMDLTNAKGYRSRRVGVHSTKPTVYAGIEORFCQCGSRFHLPEFDL 129
 Db QNPICQYGGSKDLSKSDYHKRHRVCEANSKTSVTVNGLEORFCQCGSRFHLSEFDD 179
 QY 130 EKSCRRLAGNERRRKPAPASISVLASRYGRIAPSLYENGDAQMGNSFLGNOEIGWPS 189
 Db GKRCRRRLAGNERRRKPAPAFYFLPGKRH-----KLRTSQDVNGKFLFENSIVLPE 232
 QY 190 S-----RTLDTVMR--RPVS---SPSQINMNVFSQGVGGRTSFSPEIMDTKL 237
 Db 233 SFGSLRYVIDEDDHRTSRLVSFKDEPTCSMPPTN--EQNS--SRTYESKPAIYSTEV 287
 QY 238 ESYKGIGD-----SNCLSLISNPHOPHNNNN-----NNNNNNNTWRASSGFG 284
 Db 288 SSIYDLHETASRSTRALSLASQOHLKFPNTTSTTTPNOVLNHSST----- 339
 QY 285 PMVTMAOPRPPASQHOYLPWVFKDNDMSFVLNIGRYTEPDNCOISSGTAMGEFEL 344
 Db 340 -----DYHQEGQLWIDPGKTNAG-----SSCKGKGTSTVDLQL 376
 QY 345 SDH--HHOSRRQYMED 358
 Db 377 SSHLQRIEQRRNYTGD 392

RESULT 13

Q9LOA4 PRELIMINARY; PRT; 378 AA.
 AC Q9LOA4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE FAN2.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shim P., Brooke S., Buehler E., Chao Q., Dunn P., Khan S., Kim C.,
 RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
 RA Hultzer L., Kremetskaia I., Lenz C., Li J., Liu S., Luros S.,
 RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
 RA Federpiel N.A., Theologis A., Ecker J.R.;
 RT "genomic sequence for Arabidopsis thaliana BAC FAN2 from chromosome
 I."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC008262; AAP27058.1;
 DR InterPro; IPR004333; SBP_plant_prot.
 DR Pfam; PF03110; SBP; 1
 SQ SEQUENCE 378 AA; 42923 MW; 0EF6AC5BD7C0DF49 CRC64;

Query Match 17.9%; Score 365.5; DB 10; Length 378;
 Best Local Similarity 32.0%; Pred. No. 4.6e-21;
 Matches 119; Conservative 36; Mismatches 132; Indels 85; Gaps 13;

QY 15 QAESGSGSTSSSSFGGLMGOKIYFE-----DGGGSGSSSGGSRNRRVGGGSGSG 69
 Db EEBEENISSSKFSSQEL--NRIDFKLSFLDIGNDDDDSSRGFALPSKSRASNLCS 108
 QY 70 QIPRCVGGGMDLTNAKGYRSRRVGVHSTKPTVYAGIEORFCQCGSRFHLPEFDL 129
 Db QNPICQYGGSKDLSKSDYHKRHRVCEANSKTSVTVNGLEORFCQCGSRFHLSEFDD 168
 QY 130 EKSCRRLAGNERRRKPAPASISVLASRYGRIAPSLYENGDAQMGNSFLGNOEIGWPS 189
 Db GKRCRRRLAGNERRRKPAPAFYFL-----PGKHKLRTSQSBFPG 209
 QY 190 S-----RTLDTVMR--RPVS---SPSQINMNVFSQGVGGRTSFSPEIMDTKLESYK 241
 Db 210 SLRYVIDEDDHRTSRLVSFKDEPTCSMPPTN--EQNS--SRTYESKPAIYSTEVSIW 264
 QY 242 GIGD-----SNCLSLISNPHOPHNNNN-----NNNNNNNTWRASSGFGPMTV 288
 Db 265 DLHETASRSTRALSLASQOHLKFPNTTSTTTPNOVLNHSST----- 312
 QY 289 TMAOPRPPASQHOYLPWVFKDNDMSFVLNIGRYTEPDNCOISSGTAMGEFELSDH- 347
 Db 313 -----DYHQEGQLWIDPGKTNAG-----SSCKGKGTSTVDLQLSSHL 353
 QY 348 --HHOSRRQYMED 358
 Db 354 QRIEQRRNYTGD 365

RESULT 14

Q9FZJ9 PRELIMINARY; PRT; 392 AA.
 AC Q9FZJ9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE F17L21.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Brooke S., Buehler E., Chao Q., Khan S., Kim C.,
 RA Shim P., Altafi H., Bei Q., Chin C., Chio J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharly N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federpiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
 I."
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.

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OM protein - protein search, using SW model

Run on: April 10, 2003, 13:50:09 ; Search time 13 Seconds

(without alignments)
1196.433 Million cell updates/sec

Title: US-09-839-185-2

Perfect score: 2040
Sequence: 1 MEMSGNSGPHGPGQAESESG.....MEDENTRAYDSSSHHTWLSL 375Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt 40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	330	16.2	171	1	SBP2_ANTMA
2	308.5	15.1	399	1	LG1_MAIZE
3	305	15.0	131	1	SBP1_ANTMA
4	160.5	7.9	1043	1	FTFPI_DROME
5	157.5	7.7	331	1	COL6_ARATH
6	152	7.5	1584	1	KYK1_DICDI
7	146	7.2	1858	1	P3K2_DICDI
8	125	6.1	647	1	KNRL_DROME
9	125	6.1	865	1	E78A_DROME
10	124	6.1	1230	1	ST20_CANAL
11	123.5	6.1	758	1	CC27_YEAST
12	123.5	6.1	779	1	SRP_DROME
13	123.5	6.1	843	1	MNB_DROME
14	123	6.0	988	1	OMB_DROME
15	122.5	6.0	1195	1	YK6_YEAST
16	122	6.0	1585	1	P3K3_DICDI
17	119.5	5.9	472	1	NU49_YEAST
18	119.5	5.9	1131	1	YAB9_YEAST
19	117.5	5.8	971	1	CLA4_CANAL
20	116	5.7	355	1	HKL6_LYCES
21	115.5	5.7	374	1	DMT1_MOUSE
22	115	5.6	448	1	AAC2_DICDI
23	114.5	5.6	589	1	SPY_DROME
24	114.5	5.6	2038	1	FSH_DROME
25	113.5	5.6	316	1	LORI_HUMAN
26	112.5	5.5	490	1	MOT3_YEAST
27	112	5.5	614	1	NRD1_HUMAN
28	111.5	5.5	758	1	YMS8_YEAST
29	111.5	5.5	666	1	YEAT_YEAST
30	111.5	5.5	989	1	PTP3_DICDI
31	111.5	5.5	2248	1	CYA1_DROME
32	111	5.4	713	1	YHC4_YEAST
33	111	5.4	1596	1	MAM_DROME

34	110.5	5.4	1905	1	TAGE_DICDI	P54683 dictyosteli
35	110	5.4	964	1	YINO_YEAST	P40467 saccharomyc
36	110	5.4	1341	1	YL78_YEAST	O05854 saccharomyc
37	109.5	5.4	593	1	K1C4_HUMAN	P13665 homo sapien
38	109.5	5.4	914	1	AZP1_YEAST	P14696 saccharomyc
39	109	5.3	362	1	AVEN_HUMAN	O9861 homo sapien
40	109	5.3	576	1	DEAF_DROME	Q24180 drosophila
41	109	5.3	823	1	SCN9_YEAST	P11792 saccharomyc
42	108.5	5.3	481	1	LORI_MOUSE	P18165 mus musculu
43	108.5	5.3	490	1	CAR3_DICDI	P35352 dictyosteli
44	108.5	5.3	708	1	GBF_DICDI	P54417 dictyosteli
45	108.5	5.3	850	1	D7_DICDI	P54682 dictyosteli

ALIGNMENTS

RESULT 1	SBP2_ANTMA	STANDARD;	PRT;	171 AA.
AC	Q38740;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Squamosa-promoter binding protein 2.			
GN	SBP2.			
OS	Antirrhinum majus (Garden snapdragon).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Lamiales; Veronaceae; Antirrhinum.			
OX	NCBI_TaxID=4151;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Snowman;			
RX	MEDLINE=96158840; PubMed=8569690;			
RA	Klein J., Saedler H., Hujsier P.;			
RT	"A new family of DNA binding proteins includes putative			
RT	transcriptional regulators of the Antirrhinum majus floral meristem			
RT	identity gene SQUAMOSA.";			
RL	Mol. Gen. Genet. 250:7-16(1996).			
CC	-1- FUNCTION: PROBABLE TRANSCRIPTIONAL FACTOR. BINDS TO THE PROMOTER			
CC	OF THE SQUAMOSA GENE.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- SIMILARITY: CONTAINS 1 SBP DOMAIN.			
CC	-----			
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CC	-----			
CC	EMBL; X92079; CAA63061.1; .			
DR	InterPro; IPR004333; SBP_plant_prot.			
DR	Pfam; PF03110; SBP; 1.			
KW	Transcription regulation; DNA-binding; Nuclear protein.			
FT	DOMAIN 27 39			
FT	DOMAIN 54 57			
FT	DOMAIN 85 159			
FT	DOMAIN 171 AA; E8B6B49415755EF CRC64;			
SQ	SEQUENCE			
Query Match	16.2%; Score 330; DB 1; Length 171;			
Best Local Similarity	63.7%; Pred. No. 4.4e-17;			
Matches	65; Conservative 5; Mismatches 28; Indels 4; Gaps 2;			
QY	46 GSGSSSGSGSNRRVRGSGSGSQIPRCQVEGCGMDLTNAKGYSHRYGVHSKTPKV 105			
DB	61 GEG---SGSGSGEKGHTSGSGGVAAQ-PCCLVENGADLRNCKKYQGRHRCVYAKAPV 116			
QY	106 TVAGIEORFCQCGSRFHQLPPEFLDKRSRRRLAGNERRRK 147			
DB	117 SVEGIMORFCQCGSRFHDLSEFDOTKRSRRRLAGNERRRK 158			

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RESULT 2
LG1_MAIZE STANDARD; PRT; 399 AA.
ID LG1_MAIZE
AC 004003;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE LIGULELESS1 protein.
GN LG1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22; Tissue=leaf;
RX MEDLINE=97230364; PubMed=9119226;
RA Moreno M.A., Harper L.C., Krueger R.W., Dellaporta S.L., Freeling M.;
RT "Liguleless encodes a nuclear-localized protein required for
RT induction of ligules and auricles during maize leaf organogenesis.";
RL Genes Dev. 11:616-628 (1997).
CC -1- FUNCTION: INVOLVED IN THE FORMATION OF LIGULES AND AURICLES DURING
CC LEAF ORGANOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: LEAF LIGULAR REGION, BLADE AND SHEATH.
CC LEVELS IN VERY YOUNG LIGULES AND AURICLES. PRESENT PRE- AND POST-
CC -1- SIMILARITY: CONTAINS 1 SBP DOMAIN.
CC -----
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CC -----
DR EMBL; U89496; AAB51071.1;
DR InterPro; IPR004333; SBP_plant_prot.
KW Nuclear protein; Developmental protein.
FT DOMAIN 243 259 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 185 260 SBP.
FT SEQUENCE 399 AA; 43367 MW; 1E89F304232D7B8C CRC64;
SQ
Query Match 15.1%; Score 308.5; DB 1; Length 399;
Best Local Similarity 31.4%; Pred. No. 3.9e-15;
Matches 86; Conservative 32; Mismatches 91; Indels 65; Gaps 9;
OY 21 STBES--SFSFG--GLMFGQKITYEDGGSGSSSGSRNRVRGGSGSGQIPRCQ 75
DB 146 SBAENMASFAATOLGLNIGYRTYFPPRGYT-----XGHPHPRCQ 186
OY 76 VEGCGMDLTNAKGYSRHRCVGHSTP-KYTVAGIEORFCQCGSRFHQLEPDLKRSK 134
DB 187 AEGCADSSARRYRRKVCHEHSKAPVVTAGLHQCFCCQCSFHLDLFDKASC 246
OY 135 RRLAGHNRERRRPOP-----ASLSVLSRYGRIAPSLYENDAGMNGSFLGN 182
DB 247 RRLADHNRRRKSKPSDADGDKRAHANKAAAKDKAKSSSKMDIGD-GLGAGIIGS 305
OY 183 GEIGPSSRTLDTRVMRRPVSSPSWQIN-----PMNVFGGSGVGGGTSSSPINDT 235
DB 306 ALLSKROQITMLGKRVKAVPKKASWQOHYGFPHSSSAGSGFPQTQAVSS----- 359
OY 236 KLESYKIGDSNCALSLSNP-----HOPHDNNN 264
DB 360 -----DTTSNIGQVOEPLGLGFHHQHSHN 384

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RESULT 3
SBP1_ANTMA STANDARD; PRT; 131 AA.
ID SBP1_ANTMA
AC Q38741;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Squamosa-promoter binding protein 1.
GN SBP1.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Snowman;
RX MEDLINE=96158840; PubMed=8565690;
RA Klein J., Saeedler H., Hulsner P.;
RT "A new family of DNA binding proteins includes putative
RT transcriptional regulators of the Antirrhinum majus floral meristem
RT identity gene SQUAMOSA.";
RL Mol. Gen. Genet. 250:7-16(1996).
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL FACTOR. BINDS TO THE PROMOTER
CC OF THE SQUAMOSA GENE.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: CONTAINS 1 SBP DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X92369; CA63113.1;
DR InterPro; IPR004333; SBP_plant_prot.
DR Pfam; PF03110; SBP; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 52 126 SBP.
FT SEQUENCE 131 AA; 14919 MW; 71DA57E150E4B23C CRC64;
SQ
Query Match 15.0%; Score 305; DB 1; Length 131;
Best Local Similarity 54.5%; Pred. No. 2e-15;
Matches 60; Conservative 12; Mismatches 28; Indels 10; Gaps 3;
OY 48 GSSSSG-----GRSNRRVRC--GGSGGSGQIPR-CVEGCGMDLTNAKGYSRHRCVCG 97
DB 16 GSGEGEEDDIDGESSKKTALTPSGKRAAGSTORSQVENCALAEKMTAKPYHRRKVC 75
OY 98 VHSKTPKTVAGIEORFCQCGSRFHQLEPDLKRSCKRRLAGHNRERRK 147
DB 76 FHAAAPVLSHGLQRFCCQCSRFHLSFDEARSSCKRRLAGHNRERRK 125

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RESULT 4
FTFL_DROME STANDARD; PRT; 1043 AA.
ID FTFL_DROME
AC P33244;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Nuclear hormone receptor FTZ-F1 (FTZ-F1 alpha).
GN FTZ-F1 OR NR5A3.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

```

RX MEDLINE=91227912; PubMed=1709303;
 RA Latorgna G., Ueda H., Clos J., Wu C.;
 RT "FTZ-F1, a steroid hormone receptor-like protein implicated in the
 RT activation of fushi tarazu.";
 RL Science 252:848-851(1991).
 RN [2]
 RP CHARACTERIZATION, AND SUBUNITS.
 RX MEDLINE=94217714; PubMed=8164672;
 RA Ohno C.K., Ueda H., Petkovich M.;
 RT "The Drosophila nuclear receptors FTZ-F1 alpha and FTZ-F1 beta
 RT compete as monomers for binding to a site in the fushi tarazu gene.";
 RL Mol. Cell. Biol. 14:3166-3175(1994).
 RN [3]
 RP CHARACTERIZATION, AND MUTAGENESIS.
 RX MEDLINE=93078768; PubMed=1448096;
 RA Ueda H., Sun G.-C., Murata T., Hirose S.;
 RT "A novel DNA-binding motif abuts the zinc finger domain of insect
 RT nuclear hormone receptor FTZ-F1 and mouse embryonal long terminal
 RT repeat-binding protein.";
 RL Mol. Cell. Biol. 12:5667-5672(1992).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=97172279; PubMed=9020363;
 RA Guichet A., Copeland J.W.R., Eridelyi M., Hlousek D., Zavorazky P.,
 RA Ho J., Brown S., Percival-Smith A., Krause H.M., Ephrussi A.;
 RT "The nuclear receptor homologue Ftz-F1 and the homeodomain protein
 RT Ftz are mutually dependent cofactors.";
 RL Nature 385:548-552(1997).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=97172280; PubMed=9020364;
 RA Yu Y., Li W., Su K., Yusa M., Han W., Perrimon N., Pick L.;
 RT "The nuclear hormone receptor Ftz-F1 is a cofactor for the Drosophila
 RT homeodomain protein Ftz.";
 RL Nature 385:552-555(1997).
 CC - FUNCTION: ACTS AS A COFACTOR TO FUSHI TARAZU (FTZ). FACILITATES
 CC THE BINDING OF FTZ TO DNA. BINDS THE SEQUENCE ELEMENT 5'-
 CC YCYGCGCR-3' IN THE ZEBRA ELEMENT OF FTZ. PROBABLY ALSO FUNCTION
 CC AS A RECEPTOR FOR A YET UNKNOWN LIGAND.
 CC - SUBUNIT: MONOMER; FORMS A COMPLEX WITH FTZ.
 CC - SUBCELLULAR LOCATION: Nuclear.
 CC - TISSUE SPECIFICITY: EXPRESSION IN THE PARASEGMENTAL PRIMORDIA
 CC OF THE EMBRYONIC BLASTODERM.
 CC - DEVELOPMENTAL STAGE: FIRST APPEARS IN BLASTODERM EMBRYOS. IT IS
 CC ABSENT IN SUBSEQUENT EMBRYO STAGES, AND THEN REAPPEARS IN LATE
 CC EMBRYOGENESIS TO BE FOUND IN LARVAE, PUPAE AND ADULTS.
 CC - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NRS SUBFAMILY.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL: M63711; AAA28542.1; -.
 CC HSSP: P19793; 2NUL.
 CC TRANSFAC: T00296; -.
 CC FlyBase: FBgn001078; ftz-fl.
 CC InterPro: IPR000536; Hormone_rec_1lg.
 CC InterPro: IPR001628; Znf_C4steroid.
 CC Pfam: PF00104; hormone_rec_1.
 CC Pfam: PF00105; zf-C4; 1.
 CC PRINTS: PR00047; STROIDFINGER.
 CC ProDom: PD000035; Znf_C4steroid; 1.
 CC SMART: SM00430; HOL1; 1.
 CC SMART: SM00399; Znf_C4; 1.
 CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Activator.
 FT DOMAIN 29 47 GLN-RICH (OPA-REPEAT).

FT DOMAIN 157 171 POLY-ASN.
 FT DOMAIN 361 367 POLY-GLN (OPA-REPEAT).
 FT DOMAIN 414 497 GLY-RICH.
 FT DNA_BIND 510 575 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 510 530 CA-TYPE.
 FT ZN_FING 546 570 CA-TYPE.
 FT DOMAIN 688 740 GLY-RICH.
 FT DOMAIN 837 879 LIGAND-BINDING (POTENTIAL).
 FT MUTAGEN 565 565 C->S: 100-FOLD LESS BINDING.
 FT MUTAGEN 581 581 R->Q: 100-FOLD LESS BINDING.
 FT MUTAGEN 584 584 R->Q: 100-FOLD LESS BINDING.
 FT MUTAGEN 585 585 M->I: 10-FOLD LESS BINDING.
 FT MUTAGEN 586 586 R->Q: 10-FOLD LESS BINDING.
 FT MUTAGEN 587 588 GG->AA: NO BINDING.
 FT MUTAGEN 589 589 R->Q: 10-FOLD LESS REDUCED BINDING.
 FT MUTAGEN 591 591 K->Q: NO EFFECT ON BINDING.
 SQ SEQUENCE 1043 AA; 110234 MW; 0C4539F94921617 CRC64;
 Query Match 7.9%; Score 160.5; DB 1; length 1043;
 Best Local Similarity 24.7%; Pred. No. 0.0004;
 Matches 91; Conservative 41; Mismatches 97; Indels 139; Gaps 23;
 QY 5 SNGSGHGRG---QAESGSGST-----ESSSFGS-----GLMFQKITYFEDGCGG 46
 DB 413 SGGGGGGGGGGNNLNGSSGSSAGCGYMLLPQAASSGNNNGNPNAGHWSGSV--GNGSGG 470
 QY 47 SGSSSGGGRNRRVRGGS---GSGGQI-----PRQVEGCG-----MDLT 84
 DB 471 AGNGAGAGNSGPNPMPGATPGHGEVYDFKLPFELCPV--CGDKVSGHYHGLTCE 528
 QY 85 NAKGYYSR-----HRVGVHKTPTKYTVAGIEGRFCQCGSRPHQLEPFLEKR 132
 DB 529 SCKGPFRTYQNKVKYTVAFERCHI-DKT-----QKRCPPYC-RFQCKLEVGMKLE 578
 QY 133 SCR--RLAGHN-----ERRRKP-----PASLVSASRG-----RIAPSLYENG 171
 DB 579 AVRRDRRRGRGRNRPYKRRKQVWRQRLAQALNSKSPDKPTPISPG-YQQA 637
 QY 172 DAGNNGSFLNNGEIGWPSRRLDTRVWRPVSPPS-----WQIN-----PNNVFS 216
 DB 638 YPNNN---IKQEIQIPVSL---TQSPDSSPSFALMLGQVNASTGVATPNNAGT 689
 QY 217 QGVGCGRTFSPEIMDTLYESYKIGISGNCALSLNSPHQPHDNNNNNNNNNT 276
 DB 690 GSGGCGGLNPPSS-----VGNG-----NSNNGSSGNNNNNST 721
 QY 277 WRASSGRG 284
 DB 722 GNGTSGGG 729
 RESULT 5
 COL6_ARATH STANDARD; PRT; 331 AA.
 ID COL6_ARATH AC Q91Q27;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Zinc finger protein conserved-like 6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetetskaya I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 RA Miltchev J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pat G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M.,
 RA Uterback T., Van Aken S., Vayenberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- SIMILARITY: BELONGS TO THE CONSTANS FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 B BOX-TYPE ZINC FINGERS.
 CC -----
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 DR EMBL, AC006434; AAF87126.1; -
 DR InterPro; IPR000315; Znf_Box.
 DR InterPro; IPR002926; Znf_Constans.
 DR Pfam; PF00643; Zf-B_box; 2.
 DR ProDom; PD007661; Znf_constans; 2.
 DR SMART; SM00336; BBOX; 2.
 DR PROSITE; PS50119; ZF-BBOX; 2.
 DR Zinc-finger, Nuclear_protein; Repeat; Multigene family.
 KM ZN_FING 5 47 B BOX-TYPE 1.
 FT ZN_FING 60 102 B BOX-TYPE 2.
 FT DOMAIN 118 126 POLY-SER.
 FT DOMAIN 228 238 POLY-ASN.
 SQ SEQUENCE 331 AA; 36633 MW; 6C2C5A4707976DEA CRC64;

Query Match 7.7%; Score 157.5; DB 1; Length 331;
 Best local similarity 25.2%; Pred. No. 0.00018;
 Matches 72; Conservative 39; Mismatches 92; Indels 83; Gaps 15;

QY 114 FCQQ-----CSFHLPEFDELEKSCRRRLAGNRRRKPQ-----PASLSVLAARYKRI 163
 DB 71 FCQQDRAILC-----KQDSSIHANHTKGRFLITGVKLSATSSVYKPT 117
 QY 164 APSLYENGDAAGNGSFLNGQEIIGWSSRTLDTRVWRAPVSSPQWQINPMNVFSSQSGVCG- 222
 DB 118 SKS-----SSSSSSNQDPSVSGSSISNPPLKPLSAPP-QSNKIQPSKINGDA 167
 QY 223 -----GRTSFSPPEIMDTK-----LES-----YKIGDSNCALSLSNPHOPHDNN 263
 DB 168 SVNQWGSTSTISEYIMDTLPGWHEVDFLDSLPPTYGFSKGGDDCVLPWM-----SPEDDN 223
 QY 264 N-----NNNNNNNNNNNTWR-ASSGFGPMVTYTMQPPAPSQOYLNPVWFKNDNDMSPV 319
 DB 224 NTKRNNNNNNNNNNNTVSLPSKNLGIWVQIPLQTLPSSTPNQYFS-----QNNN----- 272

QY 320 INIAGYTEPDNCOISSGTAMGEFELSDHHQSRQVQMDENTRAVD 365
 DB 273 IQFGWYMKETSPREVVSFAPI-----QNMKQGGN-NRWWD 307

RESULT 6
 KYK1 DICDI STANDARD; PRT; 1584 AA.
 AC P18160;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Non-receptor tyrosine kinase spore lysis A (EC 2.7.1.112) (Tyrosine-
 DE protein kinase 1).
 GN PYKA OR SPLA OR DPYK1.
 OS Dictyostelium discoideum (Slime mold).
 CC Eukaryota; Eukaryota; Dictyostelid; Dictyostelium.
 CC NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JH10;
 RX MEDLINE=97053827; PubMed=8898241;
 RA Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.;
 RT "The Dictyostelium dual-specificity kinase spla is essential for
 RT spore differentiation.";
 RL Development 122:3295-3305(1996).
 RN [2]
 RP SEQUENCE OF 1248-1584 FROM N.A.
 RX MEDLINE=90287147; PubMed=1972546;
 RA Tan J.L., Spudich J.A.;
 RT "Developmentally regulated protein-tyrosine kinase genes in
 RT Dictyostelium discoideum.";
 RL Mol. Cell. Biol. 10:3578-3583(1990).
 CC -1- FUNCTION: ESSENTIAL FOR SPORE DIFFERENTIATION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH A PEAK
 CC DURING THE MOUND STAGE OF MORPHOGENESIS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC -----
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 CC -----
 DR EMBL, U32174; AAB41125.1; -
 DR EMBL, M33785; AAA33202.1; -
 DR PIR; A35670; A35670.
 DR DictyDb; DD03010; Pyka.
 DR InterPro; IPR000715; Euk_Pkinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR003878; SPRY domain.
 DR InterPro; IPR003877; SPRY receptor.
 DR InterPro; IPR004040; STY_Pkinase.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR Pfam; PF00068; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR Pfam; PF00622; SPRY; 3.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00449; SPRY; 3.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50105; SAM DOMAIN; 1.
 KM Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
 FT DOMAIN 908 972 SAM.
 FT DOMAIN 403 420 POLY-ASN.
 FT DOMAIN 428 435 POLY-THR.
 FT DOMAIN 449 480 POLY-ASN.
 FT DOMAIN 483 491 POLY-ASN.
 FT DOMAIN 494 508 POLY-ASN.
 FT DOMAIN 512 532 POLY-ASN.
 FT DOMAIN 596 600 POLY-ASN.
 FT DOMAIN 808 811 POLY-PHE.
 FT DOMAIN 1026 1029 POLY-SER.
 FT DOMAIN 1195 1210 POLY-ASN.
 FT DOMAIN 1215 1220 POLY-GLN.
 FT DOMAIN 1224 1233 POLY-GLN.
 FT DOMAIN 1266 1274 POLY-PRO.

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FT DOMAIN 1289 1561 PROTEIN KINASE.
FT NP_BIND 1295 1303 ATP (BY SIMILARITY).
FT BINDING 1316 1316 ATP (BY SIMILARITY).
FT ACT_SITE 1417 1417 BY SIMILARITY.
FT CONFLICT 1248 1248 D -> R (IN REF. 2).
FT CONFLICT 1435 1435 V -> L (IN REF. 2).
SQ SEQUENCE 1584 AA; 174304 MW; 5D158945B08E01E3 CRC64;

Query Match 7.5%; Score 152; DB 1; Length 1584;
Best Local Similarity 20.3%; Pred. No. 0.0026;
Matches 97; Conservative 54; Mismatches 153; Indels 174; Gaps 19;

QY 4 GSNSGPHGPGQASGSGSTSSSPSGGLMG-----QKIYEDGG----- 44
DB 107 GTNNGRVYGP-----SFGSGDVVGGCGYSSSKTYLFTKNGVLYGVAQKVN 153
QY 45 -----GSS-----GSSSGGSRNRVNGSGG-----QSGQIPRCV 77
DB 154 IGLYPTVGLONPGSSVINFPGPSYRGAPKPKQSTIKDGGSSIIPEBDLIPKEE 213
QY 78 GCGMDLTNAKGYRRHRCVHSHKT-----PKVTAGIE-----ORFQCGSRPHOL 124
DB 214 VCRW--SEKMYHGHKVV--VRNRTAFPLDSPKDTIGCVATOPFGSGFCYFVYIID 269
QY 125 PEPDLKRSCHRRLAGHNERRRKQPSLSVLAARYGRIASLYENGDAGMNGSFLGN 184
DB 270 DKGL-----SIGLANLEY-----PTFY-----H 288
QY 185 IGV-PSS---RTLTRYRRRVPVSSPSWQINP-----NAVPSGSGVGGRTSPSP 232
DB 289 VGVMPRSYGYHNDGRKR-----WREPGVNEGSEYSGSYKKGDIIGGLSFTSREI 341
QY 233 MDLTLESYKIGDGN-----ALSLNPHQ----- 258
DB 342 FETKNGMTLGAFSNVGVFPFSVAFNEPGISITGVGPPKFSQVITMLKVNSTSLV 401
QY 259 .PHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 314
DB 402 PNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 461
QY 315 DMSVYLAIGRTPEDNCOISGTAMGEFELSDHHQSRQRMEDENTRAYSSSHHTN 372
DB 462 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 519

RESULT 7
PK2_DICDI STANDARD; PRT; 1858 AA.
ID PK2_DICDI STANDARD; PRT; 1858 AA.
AC P54674;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Phosphatidylinositol 3-kinase 2 (EC 2.7.1.137) (PI3-kinase)
DE (Pcdins-3-kinase) (PI3K).
DE PI3K OR PI3K2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_Taxid=44689;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=96009592; PubMed=7565716;
RA Zhou K., Takegawa K., Emr S.D., Pirel R.A.;
RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
RT discoideum: biological roles of putative mammalian p110 and yeast
RT vps34p PI 3-kinase homologs during growth and development.";
RL Mol. Cell. Biol. 15:5645-5656(1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-ID-myo-inositol = ADP +
CC 1-phosphatidy1-ID-myo-inositol 3-phosphate.
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -----
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CC -----
DR EMBL; U23477; AAA85722.1; -.
DR DictyDb; DD01100; PI3K.
DR InterPro; IPR002420; PI3K_C2.
DR InterPro; IPR000341; PI3K_ras_bind.
DR InterPro; IPR001263; PI3Ka.
DR InterPro; IPR000403; PI3_P14_kinase.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR Pfam; PF00792; PI3K_C2; 1.
DR Pfam; PF00794; PI3K_C2; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00144; PI3K_C2; 1.
DR SMART; SM00145; PI3Ka; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS00916; PI3_4_KINASE_3; 1.
DR TRANSFERASE; Kinase; Multigene family.
FT DOMAIN 34 40 POLY-GLY.
FT DOMAIN 166 172 POLY-SER.
FT DOMAIN 185 226 POLY-ASN.
FT DOMAIN 227 235 POLY-THR.
FT DOMAIN 246 253 POLY-SER.
FT DOMAIN 259 268 POLY-ASN.
FT DOMAIN 294 303 POLY-THR.
FT DOMAIN 361 364 POLY-SER.
FT DOMAIN 369 384 POLY-SER.
FT DOMAIN 425 429 POLY-GLN.
FT DOMAIN 439 444 POLY-THR.
FT DOMAIN 445 454 POLY-SER.
FT DOMAIN 562 570 POLY-GLY.
FT DOMAIN 715 727 POLY-THR.
FT DOMAIN 982 990 POLY-GLN.
FT DOMAIN 1015 1049 POLY-ASN.
FT DOMAIN 1598 1858 PI3K/PI4K.
SQ SEQUENCE 1858 AA; 203945 MW; A6C0333D4CDEA03 CRC64;

Query Match 7.2%; Score 146; DB 1; Length 1858;
Best Local Similarity 20.5%; Pred. No. 0.0082;
Matches 62; Conservative 40; Mismatches 114; Indels 86; Gaps 8;

QY 40 FEDGGGGSSSSSGGRNRRVGGGSGSQIAPRCQV-----EGCGMDLTNAKG 88
DB 28 FNSGNSNGSG---GGGGSNLSVNSGCSNNSIRKSTLMTNGLPLPSINDKELLLENSK- 83
QY 89 YSRHRCVGHSHKTPKTVAGIEORFQCGSRHQLEPEFDLEKRSCHRRLAGHNERRRK 148
DB 84 -----PKVV-----ELVTFPHKP----- 97
QY 149 QPASTSVLAARYGRIASLYEN-----GDAG-----MNGSFLGNQELGMPSSRTLDT 195
DB 98 -----LSTIHSVHNEIPPALEKEKEKELINTISNGVTYKWTALEILDSTINTPLAKRSRG 153
QY 196 RYMRPVPVSSPSWQINPMNVPSOGSGVGSGRTSFSPEIMDTKLSYKIGDSCNCAISL 255
DB 154 SIGSKPICN-----NLSSSSSSSTTATTPPTTNNNNNNNNNNNNNNNNNNNNNN 205
QY 256 PHQHDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 315
DB 206 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 265
QY 316 MS 317
DB 266 NS 267

RESULT 8

```


KNRL DROME
 ID KNRL DROME STANDARD; PRT; 647 AA.
 AC P13054; G9VPC8;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Knirps-related protein.
 GN KNRL OR NR0A2 OR CG4761.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89057149; PubMed=2848202;
 RA Oro A.E., Ong E.S., Margolis J.S., Posakony J.W., McKeown M.,
 RA Evans R.M.,
 RT "The Drosophila gene knirps-related is a member of the
 RT steroid-receptor gene superfamily.";
 RL Nature 336:493-496(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolashikov S.,
 RA Butts K.C., Bussam M.R., Boutz J., Brockstein P., Brothier P.,
 RA Chertis J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hooten D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jajuel M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei E., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazotto M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stepieton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NRO SUBFAMILY.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL: X14153; CA33365.1; -
 DR EMBL: AE003591; AAF51627.1; ALT_SEQ.
 DR PIR: S06450; S06450.
 DR HSSP: P20393; 1A6Y.
 DR TRANSFAC: T02773; -
 DR FLYBASE: FBgn001333; knrl.
 DR InterPro: IPR01628; Znf_C4steroid.
 DR Pfam: PF00105; zfc4_1; C4steroid.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; Znf_C4steroid; 1.
 DR SMART: SM00399; Znf_C4; 1.
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Developmental protein.
 FT DNA_BIND 14 80 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 14 34 C4-TYPE.
 FT ZN_FING 51 75 C4-TYPE.
 FT DOMAIN 121 262 GLY-RICH.
 FT DOMAIN 577 597 ASN-RICH.
 SQ SEQUENCE 647 AA; 60322 MW; E466FA081DAACDC8 CRC64;
 Query Match 6.1%; Score 125; DB 1; Length 647;
 Best Local Similarity 21.5%; Pred. No. 0.08;
 Matches 89; Conservative 42; Mismatches 139; Indels 144; Gaps 18;
 Oy 1 MEMSNSGPHGPGQAGSAGSGSTSSSPSGGLMGFGQKTYFPDGGSGSSGSGSRNRY 60
 Db 191 VEYSHKRPVAVSVSSPDHNSDSSVEVSVKGNPULHGGKNSGSSGADGSH- 248
 Oy 61 RGGSGSGSGGQIPRCVSGCGMDLTN-----AKGY----- 89
 Db 249 SCGGGGGGGGGVTTPRPPQMRKDSPLPLPRGLASMPVMPAPLPPSHLLFFGYPAL 308
 Oy 90 YSRHRCVGHSTKPK-----VTVAGIE-----QRFQCGSRF--HQLPFDLEKRS 133
 Db 309 YSHIQ--GLKPTPEQOQAAVAAVHVLFNSSGAGORFPGTSPFANHQQHKEEQPA 366
 Oy 134 CRRLLAGH-----NEBRKRKPPA-----SLVL 156
 Db 367 PARSPSTHANNHLLTNGCAADLTFRPYDLAVKSGQSGSPPTTKLPSPHSKDYISAL 426
 Oy 157 A---SRYRIAPSYEN-----GDAGMGSFYGNOEIGW-----PSSRTLDTRV 197
 Db 427 VTPNSESREHVKRQNEDEDEARADGIDGAHDEDEEDLVSMTPRHSPAQGEERTPA 486
 Oy 198 MRPVSPSPQINPMNVFSGSVGGRTS-FSSPEI-----MDTKLESTYKG 242
 Db 487 GEDPRPSPG-QDNIDIL-SMKTSSSLSSKSSPEIEPTEISSDVEKNDTDDDEDLKV 544
 Oy 243 IGDSCALSLSNP-----HOPHDNN--NNNNNNNNNT 276
 Db 545 TPBEISYRETADEIEDHSSSTETETAKTSTIENTNNNNNISNNNNNNNS 598
 RESULT 9
 E78A DROME STANDARD; PRT; 865 AA.
 ID E78A DROME STANDARD; PRT; 865 AA.
 AC P45447; O18395; O18396; G9VPC4;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ecdysone-induced protein 78C (DR-78).
 GN EIP78C OR NR1E1 OR CG18023.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, FUNCTION, AND INDUCTION.
RC STRAIN=Canton-S; TISSUE=Pupaee, and Larva;
RA MEDLINE=94006562; PubMed=8402914;
R Stone B.-U., Thummel C.S.;
RT "The Drosophila 78C early late puff contains E78, an ecdysone-
inducible gene that encodes a novel member of the nuclear hormone
receptor superfamily";
RL Cell 75:307-320(1993).
RN [21]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RC STRAIN=Canton-S; TISSUE=Pupaee;
RX MEDLINE=97032934; PubMed=8878682;
RA Russell S.R.H., Heimbeck G., Goddard C.M., Carpenter A.T.C.,
R Ashburner M.;
RT "The Drosophila Efp78C gene is not vital but has a role in regulating
chromosome puffs";
RL Genetics 144:159-170(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chamee P., Pfeiffer B.D.,
R Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Ayrl J.P., Agbayani A., An H.-D., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R Beeson K.Y., Berens P.V., Bernick B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck B.J., Brokstein P., Brotlier P.,
R Burks K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke Z., Davenport L.B., Davies P.,
R de Pablo E., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
R Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R Liu-X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
R Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
R Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
R Shue B.C., Siden-Kiamos I., Stimpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Steplenson M., Strong R., Sun E.,
R Svaydas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
R Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zavert J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE OF 321-433 FROM N.A. (ISOFORM A).
RX MEDLINE=94060116; PubMed=8241281;
RA Martin-Blanco E., Kornberg T.B.;
RT "R-78, a novel Drosophila melanogaster genomic DNA fragment highly
homologous to the DNA-binding domain of thyroid hormone-retinoic
acid-vitamin D receptor subfamily";
RL Biochim. Biophys. Acta 1216:339-341(1993).
RN [5]
RP FUNCTION: INDUCES THE EARLY LATE PUFF 78C WHICH TRIGGERS PUPARIUM
FORMATION AND DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: A/E78A (shown here) and B/E78B;
CC may be produced by alternative splicing.
CC -1- DEVELOPMENTAL STAGE: Isoform A is expressed only in mid-pupal

CC	scrapes, while isoform B is maximally expressed in newly formed prepupae and immediately following isoform A in mid-pupae.
CC	-1- INDUCTION: Both isoforms require ecdysone for activity. Isoform B also requires ecdysone-induced proteins for maximal expression.
CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC	NH1 SUBFAMILY.
CC	-1- CAUTION: Ref.2 sequence differs from that shown due to framehifts in positions 567 to 625.
CC	-1- CAUTION: Ref.3 sequence differs from that shown due to erroneous gene model prediction.
CC	-----
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CC	or send an email to license@iesb-sib.ch).
CC	-----
DR	EMBL; U01087; AAA19975.1; -
DR	EMBL; U01088; AAA19976.2; -
DR	EMBL; X98881; CAA67384.1; ALT FRAME.
DR	EMBL; X98882; CAA67385.1; ALT FRAME.
DR	EMBL; AE003593; AAF51692.1; ALT_SEQ.
DR	EMBL; X73045; CAA51523.1; -
DR	HSSP; P20393; 1A6Y.
DR	TRANSFAC; T02743; -
DR	FLYbase; FBgn0004865; Eip78C.
DR	InterPro; IPR000536; Hormone_rec_1lg.
DR	InterPro; IPR001723; Strdhmn_receptor.
DR	InterPro; IPR001628; Znf_C4steroid.
DR	Pfam; PF00104; hormone_rec1.
DR	Pfam; PF00395; z1-C4; 1.
DR	PRINTS; PR00398; STRDHOMONER.
DR	PRINTS; PR00047; STROIDFINGER.
DR	ProDom; PD000035; Znf_C4steroid; 1.
DR	SMART; SM00430; HOL1_1.
DR	SMART; SM00399; Znf_C4; 1.
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW	Transcription regulation; DNA-binding; Nuclear protein; Metal-binding; Zinc; Zinc-finger; Alternative splicing.
FT	DNA BIND 367 432
FT	FT ZN_FING 367 387
FT	FT ZN_FING 403 427
FT	DOMAIN 64 80
FT	DOMAIN 182 188
FT	DOMAIN 192 202
FT	DOMAIN 240 247
FT	DOMAIN 271 279
FT	DOMAIN 312 315
FT	DOMAIN 321 333
FT	DOMAIN 336 339
FT	DOMAIN 346 349
FT	DOMAIN 354 357
FT	DOMAIN 481 486
FT	DOMAIN 490 500
FT	DOMAIN 546 554
FT	DOMAIN 546 554
FT	VARSPLIC 2
FT	CONFLICT 39 40
FT	CONFLICT 75 78
FT	CONFLICT 321 331
FT	CONFLICT 325 326
FT	CONFLICT 430 430
FT	CONFLICT 433 433
FT	CONFLICT 502 502
FT	CONFLICT 502 502
FT	CONFLICT 515 515
FT	CONFLICT 733 733
SO	SEQUENCE 865 AA; 96024 MW; A52734720AFBA492 CnC64;
Query March	6.1%; Score 125; DB 1; Length 865;
Matches 78; Conservative	21.0%; Pred. No. 0.11; Mismatches 115; Indels 136; Gaps 15;

RA Lamb J.R., Michaud W.A., Sikorski R.S., Hieter P.A.;
 RT "Cdc16p, Cdc23p and Cdc27p form a complex essential for mitosis.";
 RL EMBL J. 13:4321-4328(1994).
 CC -1- FUNCTION: EXECUTES ESSENTIAL MITOTIC FUNCTIONS NEAR THE
 CC METAPHASE/ANAPHASE TRANSITION.
 CC -1- SUBUNIT: CDC16, CDC23 AND CDC27 FORMS A MACROMOLECULAR COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE CDC27/NUC2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 8 TPR REPEATS.
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 CC -----
 DR EMBL; X79489; CAAS6022.1; ALT_INIT.
 DR EMBL; Z35845; CAAS4905.1; -.
 DR PIR; S45825; S45825.
 DR SGD; S0000180; CDC27.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR; 8.
 DR SMART; SM00028; TPR; 5.
 DR Cell division; Cell cycle; Mitosis; Repeat; TPR repeat;
 KM Nuclear protein.
 FT REPEAT 154 187 TPR 1.
 FT REPEAT 472 505 TPR 2.
 FT REPEAT 540 573 TPR 3.
 FT REPEAT 575 607 TPR 4.
 FT REPEAT 608 641 TPR 5.
 FT REPEAT 643 675 TPR 6.
 FT REPEAT 676 709 TPR 7.
 FT REPEAT 711 743 TPR 8.
 FT DOMAIN 358 391 ASN-RICH.
 FT MUTAGEN 613 613 G->D: IN TEMPERATURE SENSITIVE MUTANT.
 SQ SEQUENCE 758 AA; 85436 MW; 8612BA4504327A02 CRC64;
 Query Match 6.1%; Score 123.5; DB 1; Length 758;
 Best Local Similarity 20.3%; Pred. No. 0.12; Indels 79; Gaps 5;
 Matches 47; Conservative 30; Mismatches 76;
 QY 141 HNEERRKROPASLTVLSRYGRAPSLYENGDAAGNGSFLNGQETIGMPSRTLDTRVWR 200
 DB 218 HNNNAASSPFS--TSLSFEPRSQPSLYSKTKNGNNNNNNNTLTFSSNS----- 267
 QY 201 PVSSPSMQINPMNVFSGQSVGGRTSPSPIMDTKLESYKIGD-----SNCAISL 253
 DB 268 PPTSSASSFSFIQHSRQOQOQANTSIKTKQNTQTEKPNALNSKTSALPNNISMLV 327
 QY 254 S-----NPHQHDNN 284
 DB 328 SPSSKQPTISSLAKYNNKLLTTPPSKLLNDRHQQNNNNNNNNNNNNNNNNNNNN 379
 QY 285 PMVTMAQPPAPSOHQYLNPMVFKDNDMSPVYLNGRTEPDNCOISSG 336
 DB 380 -----NN 406
 RESULT 12
 SRP_DROME STANDARD; PRT: 779 AA.
 AC PS2172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Box A-binding factor (ABF) (Serpin protein) (GATA-binding factor-B)
 DE (transcription factor GATA-B) (GATA-B).
 GN SRP OR ABF.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9424445; PubMed=8187633;
 RA Abel T., Michelson A.M., Maniatis T.;
 RT "A Drosophila GATA family member that binds to Adh regulatory
 RT sequences is expressed in the developing fat body."
 RL Development 119:623-633(1993).
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTIONAL ACTIVATOR PROTEIN AND
 CC MAY PLAY A KEY ROLE IN THE ORGANOGENESIS OF THE FAT BODY. BINDS A
 CC SEQUENCE ELEMENT (5'-(TA)GATA-3') FOUND IN THE LARVAL PROMOTERS
 CC OF ALL KNOWN ALCOHOL DEHYDROGENASE (ADH) GENES; ACTS AS A HOMEOTIC
 CC GENE DOWNSTREAM OF THE TERMINAL GAP GENE HKB TO PROMOTE
 CC MORPHOGENESIS AND DIFFERENTIATION OF ANTERIOR AND POSTERIOR
 CC MIDGUT.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: INITIALLY OBSERVED IN THE ANALGEN OF
 CC THE ANTERIOR AND POSTERIOR MIDGUT AND THE CEPHALIC MESODERM. IT IS
 CC FOUND IN BOTH THE ENDODERMAL AND MESODERMAL GERM LAYERS AND FOR A
 CC BRIEF PERIOD DURING GASTRULATION IT IS EXPRESSED IN THE
 CC AMIOSETEROSA. DURING GERM BAND RETRACTION IT BECOMES RESTRICTED TO
 CC THE FAT BODY.
 CC -1- SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL; X76217; CAAS3807.1; -.
 DR HSSP; P17678; IGAT.
 DR FlyBase; FBgn0003507; srp.
 DR InterPro; IPR000679; Znf_GATA.
 DR Pfam; PF00320; GATA; 1.
 DR PRINTS; PR00619; GATAZNFINGER.
 DR SMART; SM00401; ZNF_GATA; 1.
 DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
 DR PROSITE; PS50114; GATA_ZN_FINGER_2; 1.
 DR Transcription regulation; Activator; DNA-binding; Zinc-finger;
 KM Nuclear protein; Developmental protein.
 FT ZN FING 319 343 GATA-TYPE.
 FT DOMAIN 52 55 POLY-ALA.
 FT DOMAIN 62 71 POLY-ALA.
 FT DOMAIN 81 86 POLY-GLN.
 FT DOMAIN 132 137 POLY-GLY.
 FT DOMAIN 206 215 POLY-ALA.
 FT DOMAIN 254 257 POLY-GLY.
 FT DOMAIN 439 445 POLY-GLN.
 FT DOMAIN 482 487 POLY-GLN.
 FT DOMAIN 539 545 POLY-ASN.
 FT DOMAIN 550 557 POLY-ASN.
 FT DOMAIN 578 585 POLY-SER.
 FT DOMAIN 602 614 POLY-ALA.
 FT DOMAIN 700 714 POLY-GLN.
 FT DOMAIN 739 744 POLY-GLN.
 SQ SEQUENCE 779 AA; 82109 MW; 7D4AD12A241E986D CRC64;
 Query Match 6.1%; Score 123.5; DB 1; Length 779;
 Best Local Similarity 21.9%; Pred. No. 0.13; Indels 105; Gaps 16;
 Matches 75; Conservative 41; Mismatches 122;
 QY 16 AESGSGSTESSFSGIMFOQKIYFEDGGGSGSSGSGSRNRVRG-----GS 65
 DB 239 AESGSDPYKPSFNVG-----GGGSKANTSGAASVSCPSNATSAVAS 287
 QY 66 GSGQIRCOVEGGMULTYAKGYSHRV---CG-----VSKTPKTVAGIBRPFQOC 118
 DB 288 GTAATAATLIDE--HVSRAISRRLSASKRAGLSCNCHTTHSLMRNPG--BPVCNAC 343

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QY 119 S---RFHOLPE-FDLEKSCRRRLAGHNERRRKPPOPASLSVLASRYGRIAPSLYNGDAG 174
DQ 344 GLYKTLHSVPRPLTKMKDITQK-----RKRRPKGTSEKSKSKALNALIMSGSLV 396
QY 175 MNGSLG-----NOEIGMPSRRLDTRVMRRPVPSPSMQI-----NPMNVFGSGSYGG 222
DB 397 TNCNHNAGVVLDSQMDVDMDKMPQLDLKRYNSYSQPOQQLHPOYQQQQLVADHSSAA 456
QY 223 -----GRTSFSSPEIMDTKLESY-----KGIGDSNC 248
DB 457 SSPHMGSTSL-SPSAMSQHOTHFHQOQQOQLCGMTCRPTQTCKRRSTGSSISSNR 515
QY 249 A-----LSLISNPHQPHDNNNNNN-----NNNNNNNT 276
DB 516 AACSTHPAHLPHLQHPSPHQLHNNNNNNSSLPNNNNNNNS 558

RESULT 13
MNB_DROME STANDARD; PRT; 843 AA.
AC P49657;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase minibrain (EC 2.7.1.-).
GN MNB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berlin;
RX MEDLINE=95161060; PubMed=7857639;
RA Tejedor F., Zhu X.R., Kaltenbach E., Ackermann A., Baumann A.,
RA Canal I., Heisenberg M., Fischbach K.F., Pongs O.;
RT "Minibrain: a new protein kinase family involved in postembryonic
RT neurogenesis in Drosophila."
RL Neuron 14:287-301(1995).
CC CC
CC -1- FUNCTION: ROLE IN THE SPECIFIC CONTROL OF PROPER PROLIFERATION OF
CC OPTIC LOBE NEURONAL PROGENY. MUTANTS ARE CHARACTERIZED BY A
CC SPECIFIC AND MARKED SIZE REDUCTION OF THE OPTIC LOBES AND CENTRAL
CC BRAIN HEMISPHERES BUT NO MAJOR ALTERATION IN NEURONAL ARCHITECTURE
CC CAN BE FOUND.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: IN VENTRAL NERVE CORD AND SUPRAESOPHAGEAL
CC GANGLION OF EMBRYOS. IS MOST PROMINENT IN THE MUSHROOM BODY
CC NEUROFIL AND THE OUTER PROLIFERATION CENTER OF THE OPTIC LOBES IN
CC THIRD INSTAR LARVAE.
CC -1- DEVELOPMENTAL STAGE: THE FORMS A AND C ARE PRESENT MAINLY IN
CC EMBRYOS AND PUPAE. BY CONTRAST, FORM B APPEARS TO BE EXPRESSED
CC MOST MARKEDLY IN THIRD INSTAR LARVAE AND PUPAE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MNB_DYRK SUBFAMILY.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS THE INITIATOR.
CC
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CC
CC EMBL; X70794; CAA50065.1; -
CC EMBL; X70798; CAA50068.1; -
CC EMBL; X70799; CAA50069.1; -
CC HSRP; P24941; IBIH.
CC FlyBase; FBgn0002777; mnb.
CC InterPro; IPR000719; Euk_pkinase.

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DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
DR Nuclear protein; Alternative splicing; Developmental protein;
KW Neurogenesis.
FT DOMAIN 5 11 POLY-SER.
FT DOMAIN 56 74 BIPARTITE NUCLEAR LOCALIZATION SIGNAL.
FT DOMAIN 99 419 PROTEIN KINASE.
FT NP_BIND 105 113 ATP (BY SIMILARITY).
FT BINDING 128 128 ATP (BY SIMILARITY).
FT ACT_SITE 227 227 BY SIMILARITY.
FT DOMAIN 426 427 GLY/ALA/SER-RICH.
FT DOMAIN 471 474 POLY-SER.
FT DOMAIN 471 474 POLY-SER.
FT DOMAIN 505 508 POLY-SER.
FT DOMAIN 505 508 POLY-SER.
FT DOMAIN 642 646 POLY-SER.
FT DOMAIN 642 646 POLY-SER.
FT DOMAIN 677 680 POLY-SER.
FT DOMAIN 682 692 POLY-SER.
FT DOMAIN 767 776 POLY-SER.
FT DOMAIN 825 828 POLY-SER.
FT VARSPPLIC 536 539 GLM -> DRR (IN ISOFORM B).
FT VARSPPLIC 540 540 MISSING (IN ISOFORM B).
FT VARSPPLIC 536 542 GLMHSV -> VRIIVRI (IN ISOFORM C).
FT VARSPPLIC 543 843 MISSING (IN ISOFORM C).
FT VARIANT 126 126 A -> T (IN MNB1; REDUCED BRAIN VOLUME).
SQ SEQUENCE 843 AA; 89093 MW; 4AD4EB02CDAED70E CRC64;

Query Match 6.1%; Score 123.5; DB 1; Length 843;
Best local similarity 19.7%; Pred. No. 0.14;
Matches 67; Conservative 21; Mismatches 77; Indels 175; Gaps 12;

QY 43 GCGGSGSSGCGRRRRRGSGSGSGGQIRPCQYEGCGMDLTNKKGYRRHVGYSK 102
DB 439 GAGGSGSSGAGGSSGGG-GGGLAS-----NSSGAVSSSAAAPTAT 482
QY 103 PKVTAGIEQFCCQCSRFHQLPEFDLEKSCRRRLAGHNERRRKPPOPASLSVLASRYGR 162
DB 483 AATA----- 487
QY 163 IAPSLYNGAGMNGSFLNGEIGMPSRRLDTRVMRRPVPSPMQINPMNVFGSGSYGG 222
DB 488 -----AGSSGS-----GSSVGSSSAQAQOQAMPPLPLP-LPLPPL-----AGP 526
QY 223 GRTSFSSPEIMDTKLESYKGIGDSNC-----ALSLISNPHQ----- 259
DB 527 G-----GASDQCCHGLMHSVAANAMNFSALISQSNAPPSLANS 568
QY 260 -HDNN-----NNNNNNNNNTWRASGFGPMTYMA----- 291
DB 569 HHSITSLGSLHISPTGTCCHNNNSNNNT-RHSRLYGSNMVMVGHHSNNNS 627
QY 292 -----OPPAHQHLYLNPWPVKDNDNDSP 318
DB 628 ISYPHAMECDPPQMPPPPPNGHGRVPAIMQLQPNYSAP 667

RESULT 14
MNB_DROME STANDARD; PRT; 988 AA.
AC Q24432; Q27917; Q9W4K5;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Opcomotor-blind protein (lethal(1) opcomotor-blind) (L(1) omb) (Bifid
DE protein).
GN BI OR OMB OR CG3578.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

```

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=92159016; PubMed=1741374;
 RA Pflugfelder G.O., Roth H., Poock B., Kersch S., Schwarz H.,
 RA Jonescher B., Heisenberg M.;
 RT "The lethal(1)optomotor-blind gene of Drosophila melanogaster is a
 RT major organizer of optic lobe development: isolation and
 RT characterization of the gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1199-1203(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10711132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bortone D., Botchan M.R., Bouck J., Brodeur P., Brotier P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Cantler A., Chandra I.,
 RA Cherry J.M., Chew S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iegem C.,
 RA Jalali M., Kalish F., Kappen G.H., Ke Z., Kienison J.A., Ketchum K.A.,
 RA Jallat M.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod B.P., McPherson D.,
 RA Merkulov G., Mikhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazotto M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE OF 1-447 FROM N.A., AND MUTATIONAL ANALYSIS.
 RC TISSUE=larva;
 RX MEDLINE=93261414; PubMed=8492800;
 RA Poock B., Bailes J., Pflugfelder G.O.;
 RT "Transcript identification in the optomotor-blind locus of Drosophila
 RT melanogaster by intragenic recombination mapping and PCR-aided
 RT sequence analysis of lethal point mutations."
 RL Mol. Gen. Genet. 238:325-332(1993).
 CC -1- FUNCTION: ESSENTIAL PROTEIN THAT MAY FUNCTION AS A TRANSCRIPTION
 CC REGULATOR. FLIES WITH L(1)OMV MUTATIONS SHOW SEVERE MALDEVELOPMENT
 CC OF THE OPTIC LOBES. REDUCTION IN WING SIZE AND AN INCREASED
 CC ABDOMINAL PIGMENTATION. THEY DIE DURING THE PUPAL STAGE.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: IN THIRD-INSTAR LARVAE IT IS FOUND IN THE
 CC BRAIN REGION THAT WILL DEVELOP INTO OPTIC LOBES AND MORE WEAKLY IN
 CC THE THORACIC PART OF THE VENTRAL GANGLION.
 CC -1- DEVELOPMENTAL STAGE: THE PEAK PERIODS OF EXPRESSION ARE: MID-
 CC EMBRYOGENESIS, THE SECOND DAY OF PUPAL DEVELOPMENT AND IN THE

CC ADULT.
 CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
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 DR EMBL: M61796; AAA28736.1; -
 DR EMBL: AEO03431; AAF45946.1; -
 DR EMBL: S61732; AAB26697.1; JOINED.
 DR EMBL: S61727; AAB26697.1; JOINED.
 DR EMBL: S61729; AAB26697.1; JOINED.
 DR EMBL: S61744; AAB26699.1; JOINED.
 DR EMBL: S61743; AAB26699.1; JOINED.
 DR EMBL: S61955; AAB26699.1; JOINED.
 DR HSSP: P24781; 1XBR.
 DR FLYBase: FBgn0000179; b1.
 DR InterPro: IPR001699; TF_T-box.
 DR Pfam: PF00907; T-box; 1.
 DR PRINTS: PR00937; TBOX.
 DR SMART: SM00425; TBOX; 1.
 DR PROSITE: PS01283; TBOX_1; 1.
 DR PROSITE: PS01264; TBOX_2; 1.
 DR PROSITE: PS0252; TBOX_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 FT DOMAIN 51 140
 FT DOMAIN 104 107
 FT DOMAIN 179 184
 FT DOMAIN 229 236
 FT DOMAIN 238 244
 FT DNA_BIND 332 513
 FT DOMAIN 574 577
 FT DOMAIN 607 692
 FT DOMAIN 823 831
 FT DOMAIN 910 916
 FT DOMAIN 926 966
 FT CONFLICT 10 10
 FT CONFLICT 216 216
 FT CONFLICT 511 511
 FT CONFLICT 823 823
 FT CONFLICT 976 988
 SQ SEQUENCE 988 AA; 103992 MW; 032B7A447174FC9 CRC64;
 Query Match 6.0%; Score 123; DB 1; Length 988;
 Best Local Similarity 23.3%; Pred. No. 0.18;
 Matches 48; Conservative 33; Mismatches 69; Indels 56; Gaps 9;
 QY 173 AGNNGSTLGNQELGMBSSRLDTRWRPRPVSSPQWQINPNVNSQSGVGG-----RTSF 227
 DB 48 AGSNNNNSGNTNNGNNNSNN-----NTNSNTNTNTNTNLVAVPTGGQALSPQSNH 99
 QY 228 SSPFIMDTKLESTYKIGDSICALSLSPHOPDNNNNNNNNNNNNNNNNNNTRASSGFGPMT 287
 DB 100 SSSNTTTT-----SNTNNSNNNNNNNNNNNNNNNNNNNNNNNNNNNTSQGCH---H 148
 QY 288 VTAAQPPAPASQOYINPVPVFXNDNDMSVPVNLGRYTEPDNCQISSGTAMGEFELSDH 347
 DB 149 LSTTEPSPAG--TPPPIV-----GLPPI-----PPPNNSSSSSSSNSASAAAH 193
 QY 348 --HQSRQYMEDENTRAYDSSSHT 371
 DB 194 PSHR-----PTAAHS 204
 RESULT 15
 ID YK76_YEAST STANDARD; PRT; 1195 AA.
 AC P36168;
 DT 01-JUN-1994 (Rel. 29, Created)

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DT 01-JUN-1994 (Rel. 29, last sequence update)
DE 01-FEB-1995 (Rel. 31, last annotation update)
DE Hypothetical 137.5 kDa protein in MPL1-PPC1 intergenic region.
GN YKR096W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-843 FROM N.A.
RA Baladron V., Ballesta J.P.G., Bou G., del Rey F., Esteban P.F.,
RA Garcia-Cantalejo J.M., Garcia-Ramirez J.U., Gonzalez A., Jimenez A.,
RA Revuelta J.L., Santos M.A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 737-1195 FROM N.A.
RA Gallion L., Dujon B.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO YEAST Y1151C, ALSO TO THE N-TERMINAL OF
CC YEAST ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL 1 (ALD1).
CC -----
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CC -----
CC EMBL; Z28321; CAA82176.1; -.
DR PIR; S38174; S38174.
DR SGD; S0001804; YKR096W.
KW Hypothetical protein; ATP-binding.
FT DOMAIN 210 250 ASN-RICH.
FT NP_BIND 465 472 ATP (POTENTIAL).
SQ SEQUENCE 1195 AA; 137490 MW; D7251DE0B523622 CRC64;

Query Match 6.0%; Score 122.5; DB 1; Length 1195;
Best Local Similarity 22.4%; Pred. No. 0.24;
Matches 65; Conservative 31; Mismatches 75; Indels 119; Gaps 13;

QY 82 DITNAKGYISRRHVGSHSKTPKVTAGIEQRFCCQCSRFHQLPEFDLEKRCRRRLAGH 141
DB 71 DINSSKRIRSRPRFSDIEGK-----NNDHTYPR-----RTVKE 104
QY 142 NERRRRKPPASISVLAAR-----YGRAPSLYENGDAWMNGSFLNGEIGMPSSR 191
DB 105 SEKNPSPRVSSSKRLKRENSVGTQSSALISKPSFENG-----GSTAHEK--W---- 152
QY 192 TLDTWRMRPVSSPSWQINPMNVFSQGS-----VGG--GRTSFSSEIIMD 234
DB 153 -----SPENMIRKPLNV--SGNSLAFVDAGSDEGSKSEIVGGFORKNSNGSEIND 199
QY 235 ---TKLESYKIGIDSNCLSLISNPHOPHNNNNNNNNNNNNNTWRASSGFGPWTVTM 290
DB 200 KONSARDQDFNNNGNNN-----NNNNHSSNNNDNNNNNNNDNNNNNNNSNS----- 244
QY 291 AQPPAPSGHQVQLNPPWVFKDNDNMSPLVNLGRYTEPNCQISSGTAMG 340
DB 245 -----RDNNNNNSD--DSNREENDSCKPPASIKRSG 272

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Search completed: April 10, 2003, 13:53:28
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